

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 23:58:52 ; Search time 2913 Seconds  
(without alignments)  
12837.411 Million cell updates/sec

Title: US-09-659-860a-3  
Perfect score: 2309  
Sequence: 1 gagagacgtgcacgtccca.....gattaaaaatgtgtgtctt 2309

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues  
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

EST.\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.6	1.0	45	17	AZ772088 1M0574P09
C 2	22	1.0	46	17	AZ857401 2M0162M07
C 3	22	1.0	47	17	AZ592788 1M0403P22
C 4	22	1.0	50	17	AZ458729 1M0263N06
C 5	21.8	0.9	50	9	AU103152 AU103352
C 6	21.6	0.9	40	17	AZ474054 1M0290K14

C 7	21.6	0.9	47	9	AU254247
C 8	21.4	0.9	49	9	A1350847
C 9	21	0.9	50	14	T25053
C 10	20.8	0.9	49	12	BG179823
C 11	20.8	0.9	49	14	W52971
C 12	20.6	0.9	33	17	AZ788166
C 13	20.6	0.9	41	14	H59040
C 14	20.6	0.9	43	17	AZ314208
C 15	20.6	0.9	49	9	A1973603
C 16	20.4	0.9	36	9	AU259306
C 17	20.4	0.9	46	17	TA130G070
C 18	20.4	0.9	48	12	BG667239
C 19	20.4	0.9	49	9	AA505166
C 20	20.4	0.9	50	9	AU104178
C 21	20.4	0.9	50	17	AZ617534
C 22	20.2	0.9	42	14	C01292
C 23	20.2	0.9	46	9	AA946759
C 24	20.2	0.9	46	17	AZ498067
C 25	20	0.9	38	17	AZ601365
C 26	20	0.9	41	17	AZ772635
C 27	20	0.9	46	17	AL757412
C 28	20	0.9	47	17	AZ823735
C 29	20	0.9	48	17	BH852315
C 30	20	0.9	49	17	AL755942
C 31	19.8	0.9	36	9	AU255361
C 32	19.8	0.9	39	17	AZ424159
C 33	19.8	0.9	45	9	AU267061
C 34	19.8	0.9	45	12	BF732129
C 35	19.8	0.9	45	17	AZ791851
C 36	19.8	0.9	47	17	BH853527
C 37	19.8	0.9	49	9	AU394062
C 38	19.8	0.9	50	9	AU106951
C 39	19.8	0.9	50	13	B1910989
C 40	19.6	0.8	37	9	AU265147
C 41	19.6	0.8	40	9	AA137304
C 42	19.6	0.8	43	13	B1834296
C 43	19.6	0.8	48	13	B033490
C 44	19.6	0.8	48	13	B083933
C 45	19.6	0.8	49	9	AA835093
C 46	19.6	0.8	50	9	AU103566
C 47	19.6	0.8	50	9	AU103568
C 48	19.6	0.8	50	13	B1175092
C 49	19.6	0.8	50	17	AZ950287
C 50	19.6	0.8	50	17	BH221751
C 51	19.4	0.8	37	17	BH792357
C 52	19.4	0.8	41	17	AI167547
C 53	19.4	0.8	42	9	AA581390
C 54	19.4	0.8	43	9	AA283040
C 55	19.4	0.8	44	17	AC021165
C 56	19.4	0.8	46	9	A1653818
C 57	19.4	0.8	46	14	T25667
C 58	19.4	0.8	49	14	R95088
C 59	19.4	0.8	49	17	AZ769070
C 60	19.4	0.8	50	9	AA607953
C 61	19.4	0.8	50	17	TA230E010
C 62	19.2	0.8	40	17	AL764003
C 63	19.2	0.8	41	13	B1452713
C 64	19.2	0.8	41	17	AZ951455
C 65	19.2	0.8	41	17	BH863255
C 66	19.2	0.8	44	17	BH806014
C 67	19.2	0.8	45	17	AZ602556
C 68	19.2	0.8	46	9	A1085448
C 69	19.2	0.8	46	17	BH806081
C 70	19.2	0.8	48	9	AU254949
C 71	19.2	0.8	49	12	BE916026
C 72	19.2	0.8	50	9	A1624136
C 73	19.2	0.8	50	10	AY967273
C 74	19.2	0.8	51	17	AZ486263
C 75	19	0.8	39	17	BH864196
C 76	19	0.8	43	9	AA936855
C 77	19	0.8	44	12	BG68757
C 78	19	0.8	45	17	AZ504116
C 79	19	0.8	46	9	AA828238

AU254247	AU254247
A1350847	qtl1e08.x
T25053	EST628.Huma
BG179823	602329028
W52971	zc97d11.r1
AZ788166	2M0035P03
H59040	yr40f09.s1
AZ314208	1M0030H21
A1973603	sd07b05.y
AU259306	AU259306
TA130G070	T.brucel
BG667239	DRABDB04
AA505166	aa64e04.r
AU104178	AU104178
AZ617534	1M0448C22
C01292	HUMGS000456
AA946759	oc50c05.s
AZ498067	1M0335J12
AZ601365	1M0419B07
AZ772635	1M0583L07
AL757412	Arabidops
AZ823735	2M0097N19
BH852315	SALK.0744
AL755942	Arabidops
AU255361	AU255361
AZ424159	1M0203D07
AU267061	AU267061
BF732129	EST-NGR-1
AZ791851	2M0041K20
BH853527	SALK.0770
AU394062	AU394062
AU106951	AU106951
B1910989	603069394
AU265147	AU265147
AA137304	mg80b07.r
B1834296	603084315
B033490	B033490
B083933	B083933
AA835093	ak63b06.s
AU103566	AU103566
AU103568	AU103568
B1175092	OSTR0007H7
AZ950287	2M021K17
BH221751	1006103B0
BH792357	SALK.0640
AI167547	ox67h12.s
AA581390	nd88e09.s
AA283040	ztl6d06.s
AC021165	Oryza.sat
A1653818	LY01912.x
T25667	EST00536.Eg
R95088	y45h04..s1
AZ769070	1M0569D24
AA607953	vm39h06.r
TA230E010	T.brucel
AL764003	Arabidops
B1452713	603169931
AZ951455	2M0215H22
BH863255	SALK.0935
BH806014	1008063G1
AZ602556	1M0421E20
A1085448	ow85a04.s
BH806081	1008064D1
AU254949	AU254949
BE916026	601666326
A1624136	ts26c11.x
AY967273	AY967273
AZ486263	1M0314H11
BH864196	SALK.0955
AA936855	o151b06.s
BG68757	602787589
AZ504116	1M0344K08
AA828238	ob55a07.s

C 80	19	0.8	46	9	AA916623	AA916623 om05g05.s	153	18.6	0.8	49	9	AA798166	AA798166 vx67g05.r
C 81	19	0.8	46	9	AU269071	AU269071	154	18.6	0.8	49	9	AA855774	AA855774 vw74g02.i
C 82	19	0.8	46	17	TA369E01P	TA369E01P	C 155	18.6	0.8	49	10	AV742042	AV742042 av742042
C 83	19	0.8	47	17	BH86384	BH86384 SALK_1012	C 156	18.6	0.8	49	17	A2576556	A2576556 AST-T11C0
C 84	19	0.8	49	9	AU268128	AU268128	C 157	18.6	0.8	49	17	BH791118	BH791118 SALK_0587
C 85	19	0.8	49	14	H92807	H92807 yf90a12..r1	C 158	18.6	0.8	50	9	AU103157	AU103157
C 86	19	0.8	50	9	AU107724	AU107724	C 159	18.6	0.8	50	9	AU106264	AU106264
C 87	19	0.8	50	17	A2645588	A2645588 1M0511D09	C 160	18.6	0.8	50	9	AU107722	AU107722
C 88	19	0.8	50	17	A2799040	A2799040 2M0056L09	C 161	18.6	0.8	50	17	A2621023	A2621023 1M0454C04
C 89	19	0.8	50	17	BH865442	BH865442 SALK_0985	C 162	18.6	0.8	50	17	BH865870	BH865870 SALK_1000
C 90	18.8	0.8	35	9	AU268980	AU268980	C 163	18.4	0.8	32	17	A2793379	A2793379 2M0046P01
C 91	18.8	0.8	43	17	A2486679	A2486679 1M0314B23	C 164	18.4	0.8	36	17	A2800600	A2800600 2M0058O08
C 92	18.8	0.8	40	17	BH626765	BH626765 1007112H0	C 165	18.4	0.8	41	17	BH851235	BH851235 SALK_0727
C 93	18.8	0.8	43	17	BH632224	BH632224 1007094C0	C 166	18.4	0.8	44	17	A2428520	A2428520 1M0205H10
C 94	18.8	0.8	43	17	BH632235	BH632235 1007094C0	C 167	18.4	0.8	45	17	AA722052	AA722052 zh18f01.s
C 95	18.8	0.8	44	17	A2433032	A2433032 1M0218M12	C 168	18.4	0.8	45	17	A2810468	A2810468 2M0076E02
C 96	18.8	0.8	45	17	BH632327	BH632327 1007094E1	C 169	18.4	0.8	46	14	N44233	N44233 yy31c08..r1
C 97	18.8	0.8	45	17	BH801867	BH801867 1008115E0	C 170	18.4	0.8	46	17	A2339864	A2339864 1M0071G05
C 98	18.8	0.8	46	9	A1124130	A1124130 SMOVL3CAN	C 171	18.4	0.8	46	17	AL753248	AL753248
C 99	18.8	0.8	46	17	BH798631	BH798631 1008121E1	C 172	18.4	0.8	49	9	A1205223	A1205223
C 100	18.8	0.8	46	17	BH801816	BH801816 1008115A0	C 173	18.4	0.8	49	9	R86483	R86483 RABEST057T
C 101	18.8	0.8	47	17	BH626648	BH626648 1007111G0	C 174	18.4	0.8	49	14	BQ090608	BQ090608 ku17g02.Y
C 102	18.8	0.8	47	17	BH632190	BH632190 1007094A0	C 175	18.4	0.8	50	14	R89327	R89327 yg01d05..s1
C 103	18.8	0.8	47	17	AL771893	AL771893 Arabidops	C 176	18.4	0.8	50	14	T11436	T11436 CHR90002 ch
C 104	18.8	0.8	48	12	BF159807	BF159807 601767061	C 177	18.4	0.8	50	14	T11458	T11458 CHR90024 ch
C 105	18.8	0.8	49	9	AL649742	AL649742	C 178	18.4	0.8	50	14	BH856879	BH856879 SALK_0790
C 106	18.8	0.8	49	17	A2767999	A2767999 1M0567B16	C 179	18.4	0.8	37	9	AL435659	AL435659 th35a09.x
C 107	18.8	0.8	49	17	BH624457	BH624457 1007078E1	C 180	18.2	0.8	39	14	H55136	H55136 CHR220075.C
C 108	18.8	0.8	49	17	BH855006	BH855006 SALK_0972	C 181	18.2	0.8	40	13	B1834374	B1834374 603084415
C 109	18.8	0.8	50	9	AJ500405	AJ500405	C 182	18.2	0.8	41	9	AU011117	AU011117
C 110	18.8	0.8	50	9	AU102879	AU102879	C 183	18.2	0.8	41	10	AM248967	AM248967 2819506.3
C 111	18.8	0.8	50	10	AM632974	AM632974 b102d06.x	C 184	18.2	0.8	44	10	AZ303851	AZ303851 1M0003J12
C 112	18.8	0.8	50	12	BF029726	BF029726 601556615	C 185	18.2	0.8	44	17	AZ303851	AZ303851 1M0042T12
C 113	18.8	0.8	50	13	BJ066224	BJ066224	C 186	18.2	0.8	44	17	AZ321551	AZ321551 2822175.3
C 114	18.8	0.8	50	17	BH631106	BH631106 1007096H0	C 187	18.2	0.8	46	10	AM251061	AM251061 BJ055134
C 115	18.8	0.8	50	17	BH636800	BH636800 1008013C0	C 188	18.2	0.8	46	13	BJ055134	BJ055134 BJ055134
C 116	18.8	0.8	50	17	BH636973	BH636973 1008013H1	C 189	18.2	0.8	46	14	U44363	U44363 ENU44363.A5
C 117	18.8	0.8	50	17	BH796223	BH796223 1008085F0	C 190	18.2	0.8	46	17	A2588863	A2588863 1M0397P23
C 118	18.8	0.8	50	17	BH796965	BH796965 1008086C0	C 191	18.2	0.8	47	14	D20660	D20660 HUMS01636
C 119	18.8	0.8	50	17	BH797051	BH797051 1008086F0	C 192	18.2	0.8	47	17	A2786064	A2786064 2M0030G22
C 120	18.8	0.8	50	17	BH797292	BH797292 1008087F0	C 193	18.2	0.8	48	9	AL125418	AL125418 qd93c04.x
C 121	18.8	0.8	50	17	BH797605	BH797605 1008088G1	C 194	18.2	0.8	48	9	AL187964	AL187964
C 122	18.8	0.8	50	17	BH797769	BH797769 1008095B0	C 195	18.2	0.8	48	10	AV834559	AV834559 AV834559
C 123	18.8	0.8	50	17	BH797946	BH797946 1008096F0	C 196	18.2	0.8	48	17	A2820860	A2820860 2M0093B22
C 124	18.8	0.8	50	17	BH799504	BH799504 1008109A0	C 197	18.2	0.8	49	9	AA860637	AA860637 a182d10.s
C 125	18.8	0.8	50	17	BH799566	BH799566 1008109C0	C 198	18.2	0.8	49	9	AU270766	AU270766
C 126	18.8	0.8	50	17	BH800507	BH800507 1008125B0	C 199	18.2	0.8	49	17	A2514068	A2514068 1M0360C09
C 127	18.8	0.8	50	17	BH801937	BH801937 1008122B0	C 200	18.2	0.8	49	17	AZ711132	AZ711132 1M0573002
C 128	18.8	0.8	50	17	BH802654	BH802654 1008101D0	C 201	18.2	0.8	49	17	BH847226	BH847226 SALK_0446
C 129	18.8	0.8	50	17	BH802749	BH802749 1008101H0	C 202	18.2	0.8	50	9	AU103478	AU103478
C 130	18.8	0.8	50	17	BH804538	BH804538 1008102H0	C 203	18.2	0.8	50	9	AU103770	AU103770
C 131	18.8	0.8	50	17	BH804583	BH804583 1008080C0	C 204	18.2	0.8	50	9	AU103775	AU103775
C 132	18.8	0.8	50	17	BH805635	BH805635 1008061F0	C 205	18.2	0.8	50	9	AU103983	AU103983
C 133	18.8	0.8	50	17	BH805931	BH805931 1008063B0	C 206	18.2	0.8	50	9	AU104426	AU104426
C 134	18.8	0.8	50	17	BH805953	BH805953 1008063C1	C 207	18.2	0.8	50	9	AU104428	AU104428
C 135	18.8	0.8	50	17	BH805964	BH805964 1008063D0	C 208	18.2	0.8	50	9	AU107371	AU107371
C 136	18.8	0.8	50	17	BH806092	BH806092 1008064E0	C 209	18.2	0.8	34	13	BH810113	BH810113 SALK_0409
C 137	18.8	0.8	50	17	BH806108	BH806108 1008064F0	C 210	18	0.8	35	9	AL634492	AL634492
C 138	18.8	0.8	50	17	BH806125	BH806125 1008064G0	C 211	18	0.8	35	17	AZ783571	AZ783571 2M0025O24
C 139	18.8	0.8	50	17	BH807299	BH807299 1008064G0	C 212	18	0.8	35	17	A2825655	A2825655 2M00500P3
C 140	18.8	0.8	50	17	BH807530	BH807530 1008069G0	C 213	18	0.8	37	14	AA912402	AA912402 o199g09.s
C 141	18.6	0.8	36	14	T81822	T81822 yd93g06..s1	C 214	18	0.8	37	14	N48280	N48280 yz05h11..s1
C 142	18.6	0.8	36	17	TA270H08P	TA270H08P	C 215	18	0.8	39	17	A2576137	A2576137 AST-T33E0
C 143	18.6	0.8	42	12	BG896895	BG896895 HOA58-1-H	C 216	18	0.8	40	17	AL771426	AL771426 Arabidops
C 144	18.6	0.8	42	12	BF139151	BF139151 601784191	C 217	18	0.8	41	17	AZ480317	AZ480317 1M0301B16
C 145	18.6	0.8	42	17	A2775850	A2775850 2M0009M05	C 218	18	0.8	42	17	AZ514372	AZ514372 1M0361E03
C 146	18.6	0.8	44	9	AL594306	AL594306	C 219	18	0.8	43	9	A1540308	A1540308 t934e02.x
C 147	18.6	0.8	45	2	HSN002460	HSN002460	C 220	18	0.8	43	17	AL768905	AL768905 Arabidops
C 148	18.6	0.8	46	10	AV847044	AV847044	C 221	18	0.8	44	9	AU009914	AU009914
C 149	18.6	0.8	46	13	BJ080962	BJ080962	C 222	18	0.8	44	17	AZ387197	AZ387197 1M0146O20
C 150	18.6	0.8	47	9	AU264538	AU264538	C 223	18	0.8	46	9	AL588816	AL588816
C 151	18.6	0.8	47	13	BJ039490	BJ039490	C 224	18	0.8	46	9	AL588816	AL588816
C 152	18.6	0.8	49	9	AA777336	AA777336 z192h07.s	C 225	18	0.8	46	9	AL588816	AL588816

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C 226	18	0.8	46	17	A2846167	C 299	17.8	0.8	50	9	AU104979	AU104979	AU104979
C 227	18	0.8	46	17	HSWC43F06	C 300	17.8	0.8	50	9	AU104980	AU104980	AU104980
C 228	18	0.8	46	17	TA5D04P	C 301	17.8	0.8	50	9	AU104981	AU104981	AU104981
C 229	18	0.8	47	9	AU268330	C 302	17.8	0.8	50	9	AU104985	AU104985	AU104985
C 230	18	0.8	47	9	AU270701	C 303	17.8	0.8	50	9	AU105880	AU105880	AU105880
C 231	18	0.8	47	14	D18780	C 304	17.8	0.8	50	9	AU106015	AU106015	AU106015
C 232	18	0.8	47	14	TA92A07P	C 305	17.8	0.8	50	9	AU106058	AU106058	AU106058
C 233	18	0.8	48	13	BM014534	C 306	17.8	0.8	50	9	AU107718	AU107718	AU107718
C 234	18	0.8	48	13	W10946	C 307	17.8	0.8	50	9	AU107719	AU107719	AU107719
C 235	18	0.8	49	9	A1279722	C 308	17.8	0.8	50	9	AU107720	AU107720	AU107720
C 236	18	0.8	49	12	BG723524	C 309	17.8	0.8	50	9	AU107721	AU107721	AU107721
C 237	18	0.8	49	14	B0704655	C 310	17.8	0.8	50	9	AA574989	AA574989	AA574989
C 238	18	0.8	49	17	A2852964	C 311	17.8	0.8	50	10	AA573744	AA573744	AA573744
C 239	18	0.8	50	9	AA120437	C 312	17.8	0.8	50	13	BT091761	BT091761	BT091761
C 240	18	0.8	50	9	AU103561	C 313	17.8	0.8	50	14	C92347	C92347	C92347
C 241	18	0.8	50	9	AU103562	C 314	17.8	0.8	50	17	BH644632	BH644632	BH644632
C 242	18	0.8	50	10	AU103565	C 315	17.8	0.8	50	17	A2490200	A2490200	A2490200
C 243	18	0.8	50	10	BE306432	C 316	17.6	0.8	33	17	AA680642	AA680642	AA680642
C 244	18	0.8	50	12	BG722646	C 317	17.6	0.8	35	17	A2391153	A2391153	A2391153
C 245	18	0.8	50	17	A2486573	C 318	17.6	0.8	35	17	A2463350	A2463350	A2463350
C 246	18	0.8	50	17	A2496290	C 319	17.6	0.8	35	17	A2463350	A2463350	A2463350
C 247	17.8	0.8	37	14	D19564	C 320	17.6	0.8	36	9	AU266915	AU266915	AU266915
C 248	17.8	0.8	38	17	A2471063	C 321	17.6	0.8	38	17	TA371E05Q	TA371E05Q	TA371E05Q
C 249	17.8	0.8	39	9	AU266702	C 322	17.6	0.8	40	9	AA934199	AA934199	AA934199
C 250	17.8	0.8	39	9	AU266702	C 323	17.6	0.8	40	9	AA934199	AA934199	AA934199
C 251	17.8	0.8	39	17	A2942629	C 324	17.6	0.8	41	9	AA780930	AA780930	AA780930
C 252	17.8	0.8	40	9	AA953211	C 325	17.6	0.8	41	17	A2368409	A2368409	A2368409
C 253	17.8	0.8	40	9	AU012364	C 326	17.6	0.8	41	17	A2976999	A2976999	A2976999
C 254	17.8	0.8	41	17	BH803398	C 327	17.6	0.8	42	13	B1076662	B1076662	B1076662
C 255	17.8	0.8	43	9	AA1103421	C 328	17.6	0.8	42	17	A2341847	A2341847	A2341847
C 256	17.8	0.8	43	9	AA101435	C 329	17.6	0.8	43	10	BE571395	BE571395	BE571395
C 257	17.8	0.8	43	10	AV846880	C 330	17.6	0.8	43	14	D25603	D25603	D25603
C 258	17.8	0.8	43	14	T25548	C 331	17.6	0.8	43	14	W17027	W17027	W17027
C 259	17.8	0.8	43	17	A2454974	C 332	17.6	0.8	43	17	A2620145	A2620145	A2620145
C 260	17.8	0.8	43	17	AZ830358	C 333	17.6	0.8	43	17	A2787461	A2787461	A2787461
C 261	17.8	0.8	43	17	BH790815	C 334	17.6	0.8	43	17	A2787461	A2787461	A2787461
C 262	17.8	0.8	43	17	TA319B04P	C 335	17.6	0.8	44	9	BH790170	BH790170	BH790170
C 263	17.8	0.8	44	12	BE942705	C 336	17.6	0.8	44	17	AU269694	AU269694	AU269694
C 264	17.8	0.8	45	9	AA645122	C 337	17.6	0.8	45	17	A2346764	A2346764	A2346764
C 265	17.8	0.8	45	9	AU254665	C 338	17.6	0.8	45	9	AU256617	AU256617	AU256617
C 266	17.8	0.8	45	10	AA971301	C 339	17.6	0.8	46	9	AU1033350	AU1033350	AU1033350
C 267	17.8	0.8	45	17	BH800947	C 340	17.6	0.8	46	10	AA949324	AA949324	AA949324
C 268	17.8	0.8	45	17	AA334262	C 341	17.6	0.8	46	12	HSM01225	HSM01225	HSM01225
C 269	17.8	0.8	46	17	A2496495	C 342	17.6	0.8	48	13	B1058175	B1058175	B1058175
C 270	17.8	0.8	46	17	A2514402	C 343	17.6	0.8	48	14	D18686	D18686	D18686
C 271	17.8	0.8	46	17	TA365C120	C 344	17.6	0.8	48	17	AZ333060	AZ333060	AZ333060
C 272	17.8	0.8	47	9	AU265820	C 345	17.6	0.8	48	17	AZ820741	AZ820741	AZ820741
C 273	17.8	0.8	47	10	AA956026	C 346	17.6	0.8	48	17	AL761058	AL761058	AL761058
C 274	17.8	0.8	47	17	A2464547	C 347	17.6	0.8	48	17	AL763935	AL763935	AL763935
C 275	17.8	0.8	47	17	A2784478	C 348	17.6	0.8	48	17	TA320G01P	TA320G01P	TA320G01P
C 276	17.8	0.8	48	14	R77621	C 349	17.6	0.8	49	9	A1120408	A1120408	A1120408
C 277	17.8	0.8	48	17	A2450832	C 350	17.6	0.8	49	9	A1394222	A1394222	A1394222
C 278	17.8	0.8	48	17	A2936806	C 351	17.6	0.8	49	9	AA160855	AA160855	AA160855
C 279	17.8	0.8	48	17	BH636900	C 352	17.6	0.8	49	9	AU103096	AU103096	AU103096
C 280	17.8	0.8	48	17	BH637050	C 353	17.6	0.8	49	9	AU1013252	AU1013252	AU1013252
C 281	17.8	0.8	48	17	BH801932	C 354	17.6	0.8	49	9	AU263919	AU263919	AU263919
C 282	17.8	0.8	48	17	BH801999	C 355	17.6	0.8	49	9	AA422196	AA422196	AA422196
C 283	17.8	0.8	48	17	BH847018	C 356	17.6	0.8	49	10	BE023972	BE023972	BE023972
C 284	17.8	0.8	48	17	D181D197	C 357	17.6	0.8	49	13	B1045819	B1045819	B1045819
C 285	17.8	0.8	49	9	AU268128	C 358	17.6	0.8	49	14	R86483	R86483	R86483
C 286	17.8	0.8	49	12	BE692288	C 359	17.6	0.8	50	2	HSM002448	HSM002448	HSM002448
C 287	17.8	0.8	49	14	BH034637	C 360	17.6	0.8	50	9	AA842005	AA842005	AA842005
C 288	17.8	0.8	49	14	BM889473	C 361	17.6	0.8	50	9	AU104189	AU104189	AU104189
C 289	17.8	0.8	49	17	A2845842	C 362	17.6	0.8	50	9	AU106923	AU106923	AU106923
C 290	17.8	0.8	50	9	AU011239	C 363	17.6	0.8	50	9	AU107154	AU107154	AU107154
C 291	17.8	0.8	50	9	AU102279	C 364	17.6	0.8	50	9	AU269021	AU269021	AU269021
C 292	17.8	0.8	50	9	AU102280	C 365	17.6	0.8	50	10	AA548815	AA548815	AA548815
C 293	17.8	0.8	50	9	AU102383	C 366	17.6	0.8	50	10	BE344524	BE344524	BE344524
C 294	17.8	0.8	50	9	AU103704	C 367	17.6	0.8	50	13	BM069831	BM069831	BM069831
C 295	17.8	0.8	50	9	AU103894	C 368	17.6	0.8	50	13	BM126011	BM126011	BM126011
C 296	17.8	0.8	50	9	AU104833	C 369	17.6	0.8	50	13	BM516052	BM516052	BM516052
C 297	17.8	0.8	50	9	AU104976	C 370	17.6	0.8	50	14	BQ457328	BQ457328	BQ457328
C 298	17.8	0.8	50	9	AU104978	C 371	17.6	0.8	50	14	BQ457328	BQ457328	BQ457328

372	17.4	0.8	28	17	A2387822	A2387822	1M0147D23	C 445	17.2	0.7	41	13	B1650138	B1650138	603296228
373	17.4	0.8	31	10	AM248330	AM248330	2820380.5	C 446	17.2	0.7	41	17	A2465656	A2465656	1M0277C20
374	17.4	0.8	33	17	TA80C11Q	TA80C11Q	T. brucei	C 447	17.2	0.7	41	17	BH809716	BH809716	BH809716
375	17.4	0.8	36	17	AZ314238	AZ314238	1M0030N24	C 448	17.2	0.7	41	17	BH846279	BH846279	SALK 0050
376	17.4	0.8	37	9	AA056537	AA056537	zK80a05..s	C 449	17.2	0.7	41	17	TA77D03Q	TA77D03Q	SALK 0070
377	17.4	0.8	37	9	AA056537	AA056537	nm75g02..s	C 450	17.2	0.7	42	14	T57173	T57173	yc20f12..r1
378	17.4	0.8	38	17	AZ453551	AZ453551	1M0255E06	C 451	17.2	0.7	42	17	AZ600233	AZ600233	2M0058F12
379	17.4	0.8	38	17	AZ486253	AZ486253	1M0314F11	C 452	17.2	0.7	42	17	BH604014	BH604014	1008057B0
380	17.4	0.8	39	17	BH661103	BH661103	SALK 0341	C 453	17.2	0.7	43	17	A1097835	A1097835	unef002..y
381	17.4	0.8	40	13	B1052813	B1052813	B1052813	C 454	17.2	0.7	43	13	B1916603	B1916603	603178534
382	17.4	0.8	40	17	AZ615013	AZ615013	1M0444C09	C 455	17.2	0.7	43	17	A2477149	A2477149	1M0296B05
383	17.4	0.8	40	17	AZ604734	AZ604734	2M0065F11	C 456	17.2	0.7	44	9	AU259133	AU259133	1M0259133
384	17.4	0.8	40	17	BH850913	BH850913	SALK 0720	C 457	17.2	0.7	44	14	N78262	N78262	yy76a03..r1
385	17.4	0.8	43	9	A1000712	A1000712	ov07h03..s	C 458	17.2	0.7	44	17	AZ657241	AZ657241	AZ657241
386	17.4	0.8	43	9	AU255984	AU255984	ANopheles	C 459	17.2	0.7	44	17	AZ686982	AZ686982	1M053M13
387	17.4	0.8	43	17	CNS07EPW	CNS07EPW	TA243P12P	C 460	17.2	0.7	45	17	AZ686982	AZ686982	2M0265013
388	17.4	0.8	44	9	A1357277	A1357277	gx15f01..x	C 461	17.2	0.7	45	14	T17566	T17566	mp5 v260..Th
389	17.4	0.8	44	9	AU268768	AU268768	B1050937	C 462	17.2	0.7	45	17	AZ514442	AZ514442	nv39e06..x
390	17.4	0.8	44	13	D20666	D20666	HUMS01642	C 463	17.2	0.7	45	17	AA742906	AA742906	SALK 0063
391	17.4	0.8	45	17	AZ659768	AZ659768	1M0537H24	C 464	17.2	0.7	46	10	AV947975	AV947975	z124D05..x
392	17.4	0.8	46	17	BH627765	BH627765	1M007076D0	C 465	17.2	0.7	46	10	AV947975	AV947975	AV947975
393	17.4	0.8	46	17	AZ431005	AZ431005	1M0215B15	C 466	17.2	0.7	46	14	T80450	T80450	pv08f06..r1
394	17.4	0.8	47	17	BH637261	BH637261	1008015D0	C 467	17.2	0.7	46	17	AZ333198	AZ333198	1M0062H11
395	17.4	0.8	47	17	BH792501	BH792501	SALK 0569	C 468	17.2	0.7	46	17	AZ345638	AZ345638	1M0080121
396	17.4	0.8	47	17	BH802737	BH802737	1008101H0	C 469	17.2	0.7	47	13	B1080929	B1080929	B1080929
397	17.4	0.8	47	17	BH802737	BH802737	1008101H0	C 470	17.2	0.7	47	17	AZ481968	AZ481968	1M0306110
398	17.4	0.8	47	17	TA48H05P	TA48H05P	1008071D1	C 471	17.2	0.7	47	17	AZ633335	AZ633335	1M0488B23
399	17.4	0.8	48	17	BH791466	BH791466	SALK 0600	C 472	17.2	0.7	47	17	BH850536	BH850536	SALK 0714
400	17.4	0.8	48	17	AA855774	AA855774	Arabidops	C 473	17.2	0.7	48	9	AU255227	AU255227	AU255227
401	17.4	0.8	49	9	AA912467	AA912467	cm52d02..s	C 474	17.2	0.7	48	17	AZ464204	AZ464204	1M0273A03
402	17.4	0.8	49	9	A1797571	A1797571	we89b12..x	C 475	17.2	0.7	48	17	AL763457	AL763457	Arabidops
403	17.4	0.8	49	9	AU268228	AU268228	AL648382	C 476	17.2	0.7	49	17	A1192472	A1192472	g6e5f04..x
404	17.4	0.8	49	14	C20873	C20873	HUMS000494	C 477	17.2	0.7	49	10	AM082485	AM082485	xb51d06..x
405	17.4	0.8	49	17	AZ434676	AZ434676	1M0082F12	C 478	17.2	0.7	49	12	BG409010	BG409010	gb58d05..y
406	17.4	0.8	49	17	AU102313	AU102313	1M0222F03	C 479	17.2	0.7	49	17	BH810733	BH810733	1M0062F09
407	17.4	0.8	50	9	AU103250	AU103250	1M0103851	C 480	17.2	0.7	49	17	BH849144	BH849144	SALK 0511
408	17.4	0.8	50	9	AU104488	AU104488	1M0104488	C 481	17.2	0.7	49	17	AA1680337	AA1680337	cm75608..s
409	17.4	0.8	50	9	AU105661	AU105661	1M0105661	C 482	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
410	17.4	0.8	50	9	AU107384	AU107384	1M0107384	C 483	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
411	17.4	0.8	50	9	AU107387	AU107387	1M0107387	C 484	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
412	17.4	0.8	50	9	AU107388	AU107388	1M0107388	C 485	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
413	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 486	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
414	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 487	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
415	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 488	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
416	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 489	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
417	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 490	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
418	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 491	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
419	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 492	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
420	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 493	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
421	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 494	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
422	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 495	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
423	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 496	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
424	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 497	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
425	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 498	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
426	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 499	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
427	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 500	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
428	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 501	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
429	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 502	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
430	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 503	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
431	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 504	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
432	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 505	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
433	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 506	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
434	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 507	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
435	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 508	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
436	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 509	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
437	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 510	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
438	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 511	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
439	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 512	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
440	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 513	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
441	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 514	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
442	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 515	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
443	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 516	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s
444	17.4	0.8	50	9	AU107389	AU107389	1M0107389	C 517	17.2	0.7	49	10	AA1680337	AA1680337	cm75608..s



C 518 17 0.7 40 9 AA412136  
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665	16.8	0.7	48	17	BH792188	BH792188 SALK_0629	738	16.6	0.7	43	9	AA461694	AA461694 vfp3f12.r
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667	16.8	0.7	48	17	BH853315	BH853315 SALK_0744	740	16.6	0.7	43	17	A2659678	A2659678 1M0537B15
668	16.8	0.7	48	17	AL764810	AL764810 Arabidops	741	16.6	0.7	43	17	AL768905	AL768905 Arabidops
669	16.8	0.7	48	17	HSC06F06	HSC06F06 H.sapiens	742	16.6	0.7	43	17	TA18C110	TA18C110 Arabidops
670	16.8	0.7	49	9	AI052522	AI052522 oz27f05.x	743	16.6	0.7	44	9	AA162616	AA162616 T. brucei
671	16.8	0.7	49	9	AI920810	AI920810 wns2d01.x	744	16.6	0.7	44	10	AV833320	AV833320 mn39b07.r
672	16.8	0.7	49	12	BE970036	BE970036 wx38g07.x	745	16.6	0.7	44	17	A2663219	A2663219 1M0542D17
673	16.8	0.7	49	13	BM128139	BM128139 if10b06.y	746	16.6	0.7	44	17	A2790528	A2790528 2M0039P04
674	16.8	0.7	49	14	BM889473	BM889473 laa02g05-	747	16.6	0.7	44	17	BH812977	BH812977 SALK_0635
675	16.8	0.7	49	14	H16724	H16724 ym22f11.s1	748	16.6	0.7	45	9	AU256306	AU256306 AU256306
676	16.8	0.7	49	17	AZ346760	AZ346760 1M0082F12	749	16.6	0.7	45	17	A2816546	A2816546 2M0085P16
677	16.8	0.7	49	17	AZ448959	AZ448959 1M0247R04	750	16.6	0.7	45	17	BH813741	BH813741 SALK_0652
678	16.8	0.7	49	17	AZ587341	AZ587341 1M0394O20	751	16.6	0.7	45	17	BH814414	BH814414 SALK_0681
679	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	752	16.6	0.7	45	17	AL764340	AL764340 Arabidops
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681	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	754	16.6	0.7	45	17	AU259048	AU259048 Arabidops
682	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	755	16.6	0.7	46	9	AV841944	AV841944 Arabidops
683	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	756	16.6	0.7	46	10	H95347	H95347 yu21c06.s1
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687	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	760	16.6	0.7	46	17	BH812741	BH812741 SALK_0630
688	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	761	16.6	0.7	46	17	BH812744	BH812744 SALK_0630
689	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	762	16.6	0.7	46	17	TA23A070	TA23A070 T. brucei
690	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	763	16.6	0.7	46	17	AI407507	AI407507 Arabidops
691	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	764	16.6	0.7	47	9	AU265820	AU265820 Arabidops
692	16.8	0.7	50	9	AU006647	AU006647 qw6b10.x	765	16.6	0.7	47	9	AU265830	AU265830 Arabidops
693	16.8	0.7	50	10	AV847546	AV847546 AV847546	766	16.6	0.7	47	10	AM059738	AM059738 Arabidops
694	16.8	0.7	50	10	AM333255	AM333255 SI9D3 AGS	767	16.6	0.7	47	10	AM250836	AM250836 2821228.r
695	16.8	0.7	50	13	BM142834	BM142834 rxf6d10.y	768	16.6	0.7	47	13	BJ080929	BJ080929 Arabidops
696	16.8	0.7	50	13	BM18218	BM18218 k189f07.y	769	16.6	0.7	47	13	AZ6607114	AZ6607114 1M0429G23
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701	16.8	0.7	50	17	AZ621474	AZ621474 1M0454O08	774	16.6	0.7	47	17	AZ660381	AZ660381 1M0538A16
702	16.8	0.7	50	17	AZ830260	AZ830260 2M0109I21	775	16.6	0.7	47	17	AZ660381	AZ660381 1M0538A16
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704	16.8	0.7	50	17	DR18C10T	DR18C10T Arabidops	777	16.6	0.7	47	17	AG019636	AG019636 Arabidops
705	16.8	0.7	50	17	DR24E15S	DR24E15S Arabidops	778	16.6	0.7	47	17	AL754141	AL754141 Arabidops
706	16.8	0.7	50	17	AZ650845	AZ650845 Arabidops	779	16.6	0.7	48	12	BF507210	BF507210 Arabidops
707	16.8	0.7	50	17	BI081179	BI081179 602879191	780	16.6	0.7	48	17	AZ326039	AZ326039 Arabidops
708	16.8	0.7	50	17	AZ445446	AZ445446 Arabidops	781	16.6	0.7	48	17	BH85823	BH85823 Arabidops
709	16.8	0.7	50	17	AU255377	AU255377 Arabidops	782	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
710	16.8	0.7	50	17	BU076531	BU076531 Arabidops	783	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
711	16.8	0.7	50	17	BU076531	BU076531 Arabidops	784	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
712	16.8	0.7	50	17	BU076531	BU076531 Arabidops	785	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
713	16.8	0.7	50	17	BU076531	BU076531 Arabidops	786	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
714	16.8	0.7	50	17	BU076531	BU076531 Arabidops	787	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
715	16.8	0.7	50	17	BU076531	BU076531 Arabidops	788	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
716	16.8	0.7	50	17	BU076531	BU076531 Arabidops	789	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
717	16.8	0.7	50	17	BU076531	BU076531 Arabidops	790	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
718	16.8	0.7	50	17	BU076531	BU076531 Arabidops	791	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
719	16.8	0.7	50	17	BU076531	BU076531 Arabidops	792	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
720	16.8	0.7	50	17	BU076531	BU076531 Arabidops	793	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
721	16.8	0.7	50	17	BU076531	BU076531 Arabidops	794	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
722	16.8	0.7	50	17	BU076531	BU076531 Arabidops	795	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
723	16.8	0.7	50	17	BU076531	BU076531 Arabidops	796	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
724	16.8	0.7	50	17	BU076531	BU076531 Arabidops	797	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
725	16.8	0.7	50	17	BU076531	BU076531 Arabidops	798	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
726	16.8	0.7	50	17	BU076531	BU076531 Arabidops	799	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
727	16.8	0.7	50	17	BU076531	BU076531 Arabidops	800	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
728	16.8	0.7	50	17	BU076531	BU076531 Arabidops	801	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
729	16.8	0.7	50	17	BU076531	BU076531 Arabidops	802	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
730	16.8	0.7	50	17	BU076531	BU076531 Arabidops	803	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
731	16.8	0.7	50	17	BU076531	BU076531 Arabidops	804	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
732	16.8	0.7	50	17	BU076531	BU076531 Arabidops	805	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
733	16.8	0.7	50	17	BU076531	BU076531 Arabidops	806	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
734	16.8	0.7	50	17	BU076531	BU076531 Arabidops	807	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
735	16.8	0.7	50	17	BU076531	BU076531 Arabidops	808	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops
736	16.8	0.7	50	17	BU076531	BU076531 Arabidops	809	16.6	0.7	48	17	TA175A01P	TA175A01P Arabidops

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811	16.6	0.7	50	9	AU103369	AU103369	AU103369	884	16.4	0.7	44	9	AA502639	AA502639
812	16.6	0.7	50	9	AU104425	AU104425	AU104425	885	16.4	0.7	44	9	AA613679	AA613679
813	16.6	0.7	50	9	AU104427	AU104427	AU104427	886	16.4	0.7	44	14	H55075	H55075
814	16.6	0.7	50	9	AU104430	AU104430	AU104430	887	16.4	0.7	44	17	AZ322603	AZ322603
815	16.6	0.7	50	9	AU105626	AU105626	AU105626	888	16.4	0.7	44	17	AZ445546	AZ445546
816	16.6	0.7	50	9	AU105794	AU105794	AU105794	889	16.4	0.7	44	17	AZ812569	AZ812569
817	16.6	0.7	50	9	AU105826	AU105826	AU105826	890	16.4	0.7	44	17	AZ864345	AZ864345
818	16.6	0.7	50	9	AU105827	AU105827	AU105827	891	16.4	0.7	44	17	BH846596	BH846596
819	16.6	0.7	50	9	AU105832	AU105832	AU105832	892	16.4	0.7	44	17	BH853222	BH853222
820	16.6	0.7	50	9	AU105835	AU105835	AU105835	893	16.4	0.7	44	17	BH854053	BH854053
821	16.6	0.7	50	9	AU107156	AU107156	AU107156	894	16.4	0.7	44	17	BH853222	BH853222
822	16.6	0.7	50	9	AU107376	AU107376	AU107376	895	16.4	0.7	44	17	BH854050	BH854050
823	16.6	0.7	50	9	AU107377	AU107377	AU107377	896	16.4	0.7	44	17	BH854050	BH854050
824	16.6	0.7	50	9	AU107378	AU107378	AU107378	897	16.4	0.7	44	17	BH854050	BH854050
825	16.6	0.7	50	12	BG409021	BG409021	BG409021	898	16.4	0.7	44	17	BH854050	BH854050
826	16.6	0.7	50	12	BG409128	BG409128	BG409128	899	16.4	0.7	44	17	BH854050	BH854050
827	16.6	0.7	50	12	BG409130	BG409130	BG409130	900	16.4	0.7	44	17	BH854050	BH854050
828	16.6	0.7	50	13	BH021075	BH021075	BH021075	901	16.4	0.7	44	17	BH854050	BH854050
829	16.6	0.7	50	14	BQ265202	BQ265202	BQ265202	902	16.4	0.7	44	17	BH854050	BH854050
830	16.6	0.7	50	14	BQ265202	BQ265202	BQ265202	903	16.4	0.7	44	17	BH854050	BH854050
831	16.6	0.7	50	17	AZ498776	AZ498776	AZ498776	904	16.4	0.7	44	17	BH854050	BH854050
832	16.6	0.7	50	17	AZ498776	AZ498776	AZ498776	905	16.4	0.7	44	17	BH854050	BH854050
833	16.6	0.7	50	17	AZ498776	AZ498776	AZ498776	906	16.4	0.7	44	17	BH854050	BH854050
834	16.6	0.7	50	17	BH642560	BH642560	BH642560	907	16.4	0.7	44	17	BH854050	BH854050
835	16.6	0.7	50	17	BH791853	BH791853	BH791853	908	16.4	0.7	44	17	BH854050	BH854050
836	16.6	0.7	26	17	TA127E06P	TA127E06P	TA127E06P	909	16.4	0.7	44	17	BH854050	BH854050
837	16.4	0.7	28	17	AZ345640	AZ345640	AZ345640	910	16.4	0.7	44	17	BH854050	BH854050
838	16.4	0.7	29	17	AZ828692	AZ828692	AZ828692	911	16.4	0.7	44	17	BH854050	BH854050
839	16.4	0.7	31	9	AU256721	AU256721	AU256721	912	16.4	0.7	44	17	BH854050	BH854050
840	16.4	0.7	32	14	C00058	C00058	C00058	913	16.4	0.7	44	17	BH854050	BH854050
841	16.4	0.7	33	10	AV966430	AV966430	AV966430	914	16.4	0.7	44	17	BH854050	BH854050
842	16.4	0.7	33	13	B1066158	B1066158	B1066158	915	16.4	0.7	44	17	BH854050	BH854050
843	16.4	0.7	34	17	AL757724	AL757724	AL757724	916	16.4	0.7	44	17	BH854050	BH854050
844	16.4	0.7	35	10	AV836236	AV836236	AV836236	917	16.4	0.7	44	17	BH854050	BH854050
845	16.4	0.7	35	10	AV957679	AV957679	AV957679	918	16.4	0.7	44	17	BH854050	BH854050
846	16.4	0.7	35	13	BI333189	BI333189	BI333189	919	16.4	0.7	44	17	BH854050	BH854050
847	16.4	0.7	35	14	D18224	D18224	D18224	920	16.4	0.7	44	17	BH854050	BH854050
848	16.4	0.7	35	14	D18224	D18224	D18224	921	16.4	0.7	44	17	BH854050	BH854050
849	16.4	0.7	35	17	AZ946037	AZ946037	AZ946037	922	16.4	0.7	44	17	BH854050	BH854050
850	16.4	0.7	36	10	B1078336	B1078336	B1078336	923	16.4	0.7	44	17	BH854050	BH854050
851	16.4	0.7	36	13	BI078336	BI078336	BI078336	924	16.4	0.7	44	17	BH854050	BH854050
852	16.4	0.7	36	17	AZ648412	AZ648412	AZ648412	925	16.4	0.7	44	17	BH854050	BH854050
853	16.4	0.7	36	17	AL769642	AL769642	AL769642	926	16.4	0.7	44	17	BH854050	BH854050
854	16.4	0.7	37	9	AA948700	AA948700	AA948700	927	16.4	0.7	44	17	BH854050	BH854050
855	16.4	0.7	37	14	H56911	H56911	H56911	928	16.4	0.7	44	17	BH854050	BH854050
856	16.4	0.7	37	14	T84001	T84001	T84001	929	16.4	0.7	44	17	BH854050	BH854050
857	16.4	0.7	37	17	AZ659652	AZ659652	AZ659652	930	16.4	0.7	44	17	BH854050	BH854050
858	16.4	0.7	38	13	B1078336	B1078336	B1078336	931	16.4	0.7	44	17	BH854050	BH854050
859	16.4	0.7	39	17	AZ584894	AZ584894	AZ584894	932	16.4	0.7	44	17	BH854050	BH854050
860	16.4	0.7	39	17	AZ584894	AZ584894	AZ584894	933	16.4	0.7	44	17	BH854050	BH854050
861	16.4	0.7	39	17	AZ71977	AZ71977	AZ71977	934	16.4	0.7	44	17	BH854050	BH854050
862	16.4	0.7	39	17	TA178C01Q	TA178C01Q	TA178C01Q	935	16.4	0.7	44	17	BH854050	BH854050
863	16.4	0.7	40	9	AI146712	AI146712	AI146712	936	16.4	0.7	44	17	BH854050	BH854050
864	16.4	0.7	40	9	AU254534	AU254534	AU254534	937	16.4	0.7	44	17	BH854050	BH854050
865	16.4	0.7	40	10	AV964831	AV964831	AV964831	938	16.4	0.7	44	17	BH854050	BH854050
866	16.4	0.7	40	13	B1078336	B1078336	B1078336	939	16.4	0.7	44	17	BH854050	BH854050
867	16.4	0.7	40	17	AZ511352	AZ511352	AZ511352	940	16.4	0.7	44	17	BH854050	BH854050
868	16.4	0.7	41	17	AZ646783	AZ646783	AZ646783	941	16.4	0.7	44	17	BH854050	BH854050
869	16.4	0.7	41	17	AZ646783	AZ646783	AZ646783	942	16.4	0.7	44	17	BH854050	BH854050
870	16.4	0.7	41	17	AZ646783	AZ646783	AZ646783	943	16.4	0.7	44	17	BH854050	BH854050
871	16.4	0.7	42	9	AU267242	AU267242	AU267242	944	16.4	0.7	44	17	BH854050	BH854050
872	16.4	0.7	42	13	B1078336	B1078336	B1078336	945	16.4	0.7	44	17	BH854050	BH854050
873	16.4	0.7	42	17	AZ633442	AZ633442	AZ633442	946	16.4	0.7	44	17	BH854050	BH854050
874	16.4	0.7	43	9	AI141013	AI141013	AI141013	947	16.4	0.7	44	17	BH854050	BH854050
875	16.4	0.7	43	9	AU013998	AU013998	AU013998	948	16.4	0.7	44	17	BH854050	BH854050
876	16.4	0.7	43	9	AA564874	AA564874	AA564874	949	16.4	0.7	44	17	BH854050	BH854050
877	16.4	0.7	43	10	AA833389	AA833389	AA833389	950	16.4	0.7	44	17	BH854050	BH854050
878	16.4	0.7	43	14	TA61017	TA61017	TA61017	951	16.4	0.7	44	17	BH854050	BH854050
879	16.4	0.7	43	14	W95929	W95929	W95929	952	16.4	0.7	44	17	BH854050	BH854050
880	16.4	0.7	43	17	AZ428834	AZ428834	AZ428834	953	16.4	0.7	44	17	BH854050	BH854050
881	16.4	0.7	43	17	BH638192	BH638192	BH638192	954	16.4	0.7	44	17	BH854050	BH854050
882	16.4	0.7	44	9	AA700996	AA700996	AA700996	955	16.4	0.7	44	17	BH854050	BH854050



Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0162 row: M column: 07  
Seq primer: CCGTCTAAACGACGCCGACAT  
Class: plasmid ends  
High quality sequence stop: 46.

## FEATURES

source

Location/Qualifiers  
1..46

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C2M0162M07"  
/clone\_1ib="Mouse 10kb plasmid U06C1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

1 a 23 c 0 g 22 t

## ORIGIN

Query Match 1.0%; Score 22; DB 17; Length 46;  
Best local Similarity 73.7%; Pred. No. 1.1e+06;  
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1902 GGCACAGTGGCGAGAGAACAGAAATGATGTA 1939  
DB 38 GGGAGAGAGAGTGAAGAGAGAGAGAGAGAGAA 1

## RESULT 3

A2592788

## LOCUS

47 bp DNA linear GSS 13-DEC-2000

## DEFINITION

1M0403P22R Mouse 10kb plasmid U06C1M library Mus musculus genomic

## ACCESSION

A2592788

## VERSION

A2592788.1 GI:11714978

## KEYWORDS

GSS.

## SOURCE

house mouse.

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 47)

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0403 row: P column: 22  
Seq primer: CACACAGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 47.

## FEATURES

source

Location/Qualifiers  
1..47

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C1M0403P22"  
/clone\_1ib="Mouse 10kb plasmid U06C1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

12 a 8 c 16 g 11 t

## ORIGIN

Query Match 1.0%; Score 22; DB 17; Length 47;  
Best local Similarity 67.4%; Pred. No. 1.1e+06;  
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1025 CTTGAATATTCGAAATTCCTCCAGATTTCAGGAAATG 1070  
DB 2 CCGAAGCGCTTGAGATATCTACAGCATTCGAAATTCAGGGCATG 47

## RESULT 4

A2458729/c

## LOCUS

50 bp DNA linear GSS 04-OCT-2000

## DEFINITION

1M0263N06F Mouse 10kb plasmid U06C1M library Mus musculus genomic

## ACCESSION

A2458729

## VERSION

A2458729.1 GI:10616854

## KEYWORDS

GSS.

## SOURCE

house mouse.

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 50)

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah





```

/obj_xref="taxon:9606"
/clone="IMAGE:4430262"
/clone_1ib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/site="Organ: prostate; Vector: pCW-SPOrt6; Site_1: NotI;
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

```

Sequence	Best local similarity	Score	DB	Length
142 GTCCCTCTCAGTAAAGAGAAATATCTCCACATGGCAGTC	0.9%;	20.8;	14;	49;
	66.7%;			
48 GTCCCTCTGCAGTCTCTATACCATTAATGTACCCCTGCNNTC	0;	2.1e+06;		
	0;			
SPLIT 12				
7/88166/c				
FINITION				
AZ788166	33 bp	DNA	linear	GSS 16-FEB-2001
2M0035P03F	Mouse	10kb	plasmid	U06C1M library Mus musculus genomic





REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 43) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0030 row: H column: 21 Seq primer: CACACGGAACACGTATGACC Class: plasmid ends High quality sequence stop: 43.
FEATURES	Location/Qualifiers 1..43 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="U00C1M0030H21" /clone_1lb="Mouse 10kb plasmid U00C1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114/73211419b[AR129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	14 a 13 c 2 g 14 t
ORIGIN	
Query Match	0.9%; Score 20.6; DB 17; Length 43;
Best Local Similarity	85.2%; Pred. No. 2.3e+06;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY 1978 CTCACAACTTATCCATCATCATTT 2004	
Db 17 CTCATCATTTATCCATCATCATGT 43	
RESULT 15	
AI973603/c	
LOCUS	AI973603 49 bp mRNA linear EST 30-NOV-2001
DEFINITION	sd07b05.y1 Gm-cl020 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl020-970 5' similar to TR:063545 063545 NADH DEHYDROGENASE
ACCESSION	AI973603
VERSION	AI973603.1 GI:5770429
KEYWORDS	EST.
SOURCE	soybean.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Glycine max	1 (bases 1 to 49)	Shoemaker, R., Kelm, P., Vodka, L., Erpelting, J., Corvett, V., Khanna, A., Boll, B., Mair, M., Hiller, L., Kneba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, I., Persson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., R., Watterston, R. and Wilson, R.	Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public Soybean EST Project
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots; Rosidae: eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae Glycine.					Public Soybean EST Project
					Washington University School of Medicine
					4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
					Tel: 314 286 1800
					Fax: 314 286 1810
					Email: est@watson.wustl.edu
					Trace considered overall poor quality
					Possible reversed clone: similarity on wrong strand This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800 )-533-4363 or contact via email: csh@resgen.com
					Insert length: 585 Std Error: 0.00
					Seq primer: ~40RP from Gibco
					High quality sequence stop: 1.
					Location/Qualifiers
					1..49
					Source

```

/clone="GENOME SYSTEMS CLONE ID: Gm-c1020-970"
/clone_id="Gm-c1020"
/tissue_type="root nodules of greenhouse grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from nodules on the roots of 2.5 month-old glycine max 'Williams' plants that were greenhouse grown. The cDNA library was prepared using the Stratagene pBluescript II SK(+) library construction kit. First strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (v=A, C, or G) was added to the 3' end of the primer (GAGACGACAGACGACGACGACGACGACG(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size-fractionated with a 400 bp cutoff, using a SizeStep 400 Spin column from Pharmacia. The column eluent was ligated to EcoRI adaptors and phosphorylated. The XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Predisgest vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=56) and sequence (n=16). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
```



PCR: The PCR products were separated on sequencing gel.  
The differential bands were cut, reamplified, cloned into  
pMD18-T vector and confirmed by Northern blot."

BASE COUNT 38 a 4 c 0 g 6 t

ORIGIN

Query Match 0.9%; Score 20.4; DB 12; Length 48;  
Best Local Similarity 65.2%; Pred. No. 2.7e+06;  
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1104 TGTCTTTGTCCTGATTTTCAGACTTTTATATGTTAT 1149

Db 46 TTTTGTGTTTGTGTTTGTGTTTAAAGTGTGTTTAAATTTT 1

RESULT 19  
AA505166/c  
LOCUS 49 bp mRNA linear EST 18-AUG-1997  
DEFINITION aa64e04.t1 NCI-CGAP-GCB1 Homo sapiens cDNA clone IMAGE:825726 5'

AA505166  
VERSION similar to TR:G535513 G535513 HOMOLOG OF YEAST MUTL ;, mRNA  
KEYWORDS sequence.

AA505166.1 GI:2241326  
EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 49)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLINL at:

www.bio.lnml.gov/bdrp/image/image.html

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seg primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1.49

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/db\_xref="taxon:9606"

/clone="IMAGE:825726"

/clone\_lib="NCI-CGAP GCB1"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

5'-GTGACCAATCTGAGTGGAGCGCCCTCATTTTCTTTT-3'

1. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

24 a 5 c 5 g 15 t

ORIGIN

Query Match 0.9%; Score 20.4; DB 9; Length 49;  
Best Local Similarity 71.1%; Pred. No. 2.7e+06;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 2067 AATCTGTATAGCTTAAATATATATGACACTTTT 2104

Db 48 AACTTGTGTTTCTCCTTAAATTTATTTTAAGTTT 11

RESULT 20

AU104178 50 bp mRNA linear EST 30-AUG-2001

LOCUS AU104178 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION KAT00217, mRNA sequence.

ACCESSION AU104178.1 GI:13553699

VERSION EST.

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

COMMENT

Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

Location/Qualifiers

1.50

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="KAT00217"

/clone\_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT

12 a 18 c 6 g 14 t

ORIGIN

Query Match

Best Local Similarity 65.2%; Pred. No. 2.7e+06;  
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1964

AGTAATACATGCTAACAATTTATTCATTCATCATTTATTTCA 2009

Db 1 AATTAATCCTGCTGGCCACCGCATCTACTCTACCATCTTTGCA 46

RESULT 21  
AZ617534/c 50 bp DNA linear GSS 13-DEC-2000

LOCUS 1M0448C22R Mouse 10kb plasmid U06C1M library Mus musculus genomic

DEFINITION clone U06C1M0448C22 R, DNA sequence.

ACCESSION AZ617534

VERSION AZ617534

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 50)

Dunn,D., Aoyagi,A., Barber,M., Beccorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.













Location/Qualifiers  
1. .39

Query Match	0.98;	Score 19.8;	DB 17;	Length 39;
Best Local Similarity	77.48;	Pred. No. 3.6e+06;		
Matches 24; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Oy	3	GAGACTGTGCCAGTCCCGAGCCGCTACCGC	33
Db	1	GATACCTGTCAGTCCATACCTCCCTAACAC	31

RESULT 33	LOCUS	DEFINITION
AU267061	45 bp	VS Dictyostelium discoidium cDNA clone VSH196 5', mRNA

ACCESSION	AU267061	
VERSION	AU267061.1	GI:20525859
KEYWORDS	EST.	
SOURCE	Dictyostelium discoideum	

REFERENCE  
AUTHORS  
1 (bases 1 to 45)  
Eukaryota; mycetozoa; Dictyostellida; Dictyostellum  
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai

TITLE	JOURNAL	COMMENT
Takeuchi, I., Kohara, Y. and Tanaka, Y. Population analysis of cDNAs from unicellular and multicellular stages of <i>Dictyostelium discoideum</i> unpublished (2002)		Contact: Hideko Urushihara

**FEATURES**

Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tenmoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel.: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: [hitekoboiol.tsukuba.ac.jp](mailto:hitekoboiol.tsukuba.ac.jp).  
Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .45

```

/organism="Dicyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH196"
/clone_1b="VS"
/sex="mat A"
/dev_stage="vegetative"

```

BASE COUNT	31 a	1 c	2 g	10 t	1 others
ORIGIN					

Query Match	0.98;	Score 19.8;	DB 9;	Length 45;
Best Local Similarity	75.08;	Pred. No. 3.7e+06;		
Matches 24; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

```

QY      474  ATGAGACAAGAAAATGTAATTATGGGAAGAT  50
          | | | | | | | | | | | | | | | |
Db      4    AAGGAAAATAAAATTTAATTATNCTAAAAAT  35

```

RESULT 34  
BF732129/c

LOCUS	BF732129	45 bp	linear	EST 30-MAY-2001
DEFINITION	EST-NGR-1-07 mouse GR-1+ myeloid progenitor cells			
musculus	CDNA 3', mRNA sequence.			CDNA Library Mus
ACCESSION	BF732129			

VERSION	BF732129.1	GI:14249749
KEYWORDS	EST.	
SOURCE	house mouse.	

ORGANISM	REFERENCE
Mus musculus	Chordata; Euteleostomi;
Muikuyirya	Cranata; Vertebrata;
Mammalia; Eutheria;	Sciurognathi; Muridae;
1 (bases 1 to 45)	Murinae; Mus.

POLYNOMIALS  
 CHEN, J., ROWLEY, D. A., CLARK, T., LEE, S., ZHOU, G., BEER, C., ROWLEY  
 J. D., and Wang, S. M.  
 Pattern of gene expression in mouse GR-1+ myeloid progenitor cells  
 Unpublished (2001)  
 Contact: Wang SM  
 wsm@u.washington.edu

Email: swangl@midway.uchicago.edu  
 This EST fragment was amplified from mouse GR-1+ myeloid progenitor cells DNA library with Glgi technique (Generation of Longer cDNA fragments from SAGE tags for Gene identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the last CATG site of the target cDNA sequence.  
 Seq primer: M13forward.

FEATURES	Location/Qualifiers
source	1. .45

```

/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
library"

```

```

/sex="female"
/tissue_type="bone marrow"
/cell_type="GR-1 myeloid progenitor cells"
/mouse_cDNA was identified and isolated from Mus musculus
benzo(a)pyrene-downregulated total RNA pool by
differential Display Polymerase Chain Reaction using
indicated anchor and arbitrary primer (Heteroglyph mRNA
Profile Kit 3, Genomex Corporation, Foster City, CA) and
sequenced directly from PCR products.

```

BASE COUNT	9 a	8 c	4
ORIGIN			

Query Match	0.98;	Score 19.8;	DB 12;	Length 45;
Best Local Similarity	69.28;	Pred. No. 3.7e+06;		
Matches 27; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

OY 1430 TTTCATGCAAAAGTCTCATATAGATTAGACGAGAAAAA 1468  
| | | | |  
Db 41 TTTCAAGTAAGAAGTCTCGGATGTGAAAAAAAAAAAAAAAA 3

RESULT 35	45 bp	DNA	linear	GSS 16-FEB-2001
AZ791851/c				
INOCUS				
AZ791851				







[illegible]

```

Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
    source
        1..48
            /organism="Xenopus laevis"
            /db_xref="taxon:8355"
            /clone_lib="XL086K08"
            /clone_lib=NIDB Mochii normalized Xenopus tailbud library"
            /tissue_type="whole embryo"
            /dev_stage="stage 25"
            /note="Vector: pBSRN3; site_1: NotI; site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute) "

BASE COUNT
    BASE COUNT      8 a          1 c          11 g          23 t          5 others

ORIGIN
Query Match              0.8%; Score 19.6; DB 13; Length 48;
Best Local Similarity   60.9%; Pred.No.4.2e+06;
Matches 28; Conservative 0; Mismatches 18; Indels 0; Gaps 0.

QY 1091 AAC TTC TG GT C CT G T C T T T T T C T C T C G A A T T T T C A G A C A C T T T T 1136
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AAATTTTNGGGGGGCGTTTTTTTTTTTTTTGGGGNTTCNMAAATTTT 46

RESULT 45
AAC835093/c LOCUS
DEFINITION AAC835093 49 bp mRNA linear EST 23-FEB-1998
IMAGE:1412513 3' similar to gb:X72781 TRYPINOGEN IVA PRECURSOR (HUMAN);, mRNA sequence.
VERSION AAC835093
KEYWORDS AAC835093.1 GI:2908821
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G.P., Marra,M., Martin
White,Y., Wylie,T., Waterston,R. and Wilson,R.
J. Moore,B., Schellenberg,K., Stepien,M., Tan,F., Theisling,B.,
WashU-NCI human EST project
Unpublished (1997)
Contact: Wilton RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the
Seg Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. EM from Amersham.

FEATURES
    source
        1..49
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1412511"
            /clone_lib="Barstead pancreas HPLRBI"
            /sex="female"
            /dev_stage="adult, 34 years"
            /lab_host="DH10B"
            /note="Organ: pancreas; Vector: pTY73D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(ct) primer
[5',
TGCTAGCAACTGAAGTGGAGGCCGCCCTTTTGTTTTGTTTTGTTTTGTTTTGTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors

```

[AATGCGATCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector.  
Library constructed by Bob Barstead."

BASE COUNT 12 a 7 c 16 g 14 t

Query Match 0.8%; Score 19.6; DB 9; Length 49;  
Best Local Similarity 66.7%; Pred. No. 4.2e+06;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 142 GTCCCTCTCAGTAAGAAGAAAATGTCACATGCGATC 183

Db 48 GTCCCTCTCAGTCTATACCAATTAAGTACCCTGCTCTC 7

RESULT 46  
AUI03566/c 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AUI03566 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION HEP17402, mRNA sequence.  
ACCESSION AUI03566  
VERSION AUI03566.1 GI:13553087  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

TITLE EMB0 Rep. 2 (5), 388-393 (2001)

JOURNAL  
MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source 1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HEP17402"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated U937 cells"

BASE COUNT 16 a 15 c 9 g 10 t

ORIGIN

Query Match 0.8%; Score 19.6; DB 9; Length 50;  
Best Local Similarity 73.5%; Pred. No. 4.2e+06;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1455 TTAGAGGAGAAAAGCTTAATGATCTGATATGT 1488

Db 44 TTGGCGGAGCTAAAGCTAGTGTCTGAGAGT 11

RESULT 47  
AUI03568/c 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AUI03568 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION HEP21445, mRNA sequence.  
ACCESSION AUI03568  
VERSION AUI03568.1 GI:13553089  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL  
MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source 1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HEP21445"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated U937 cells"

BASE COUNT 13 a 16 c 7 g 14 t

ORIGIN

Query Match 0.8%; Score 19.6; DB 9; Length 50;  
Best Local Similarity 73.5%; Pred. No. 4.2e+06;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1455 TTAGAGGAGAAAAGCTTAATGATCTGATATGT 1488

Db 50 TTGGAGGAGCTAAAGCTGTAATCTGAGAGT 17

RESULT 48  
B1175092 50 bp mRNA linear EST 09-JUL-2001  
LOCUS B1175092  
DEFINITION OSTR007H\_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to  
F59A2.5, mRNA sequence.  
ACCESSION B1175092  
VERSION B1175092.1 GI:14640895  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiodea  
1 (bases 1 to 50)  
Rhabditiidae; Peleodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 50)  
Jackson,C., Shin-I,T., Tzelias,N., Thierry-Mieg,N., Moore,T.,  
Reboul,J., Vaglio,P., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,  
Lee,H., Hittl,J., Doucet-Stamm,L., Hartley,J.L., Temple,G.F.,  
Brasch,M.A., Vandenhoute,J., Lamesch,P.E., Hill,D.B. and Vidal,M.  
Open-reading-frame sequence tags (OSTs) support the existence of at  
least 17,300 genes in C. elegans  
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL  
MEDLINE 21135099  
COMMENT Contact: Reboul J, Vaglio P  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
44 Binney Street, Boston, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 2425  
Email: Jerome.Reboul@dfci.harvard.edu  
Sequence tag of gateway entry clones. The primers used were  
designed on the predicted protein encoding ORF. C. elegans ORFome  
cloning project; Contact: jerome\_reboul@dfci.harvard.edu or  
philippe\_vaglio@dfci.harvard.edu  
POLYA-NO.

FEATURES  
source 1..50  
Location/Qualifiers

ORGANISM	"Caenorhabditis elegans"
/strain="N2"	
/db_xref="taxon:6239"	
/clone_lib="AD-wrmcDNA"	
/sex="Hermaphrodite and male"	
/tissue_type="whole animal"	
/dev_stage="mixed stage"	
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"	
BASE COUNT	9 a 12 c 4 g 25 t
ORIGIN	
Query Match	0.8% Score 19.6; DB 13; Length 50;
Best Local Similarity	66.7%; Pred. NO.4.2e+06;
Matches	28: Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy	1393 TGTGATTGTAATGATTTTCATTTGCGCTAGGCGACGATTTTCA 1434
Db	1 TTTCTTTTCATCGCTTTCTTCGATTTTCCACGATTTTCA 42
DEFINITION	50 bp DNA Linear GSS 27-APR-2001
LOCUS	A2950287
ACCESSION	2M0214K17F Mouse 10kb plasmid U06C2M library Mus musculus genomic
VERSION	A2950287
KEYWORDS	A2950287.1 GI:13821514
SOURCE	GSS.
ORGANISM	house mouse.
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 50)	
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,	
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly	
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.	
and Wright,D., Weiss,R.	
Mouse whole genome scaffolding with paired end reads from 10kb	
plasmid inserts	
Unpublished (2000)	
Contact: Robert B. Weiss	
University of Utah Genome Center	
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT	
84112, USA	
Tel: 801 585 5606	
Fax: 801 585 7177	
Email: ddunn@genetics.utah.edu	
Insert Length: 10000 Std Error: 0.00	
Plate: 0214 row: K column: 17	
Seq primer: CGTGTAAACGACGCGCAG	
Class: plasmid ends	
High quality sequence stop: 50.	
Location/Qualifiers	
1..50	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="U06C2M0214K17"	
/clone_lib="mouse 10kb plasmid U06C2M library"	
/sex="Female"	
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"	
/note="Vector: PWD42nv; Purified genomic DNA from M.	
musculus C57BL/6J (female) was obtained from the Jackson	
Laboratory Mouse DNA Resource	
(http://www.jax.org/resources/documents/dnares/). The DNA	
was hydrodynamically sheared by repeated passage through a	
0.005 inch orifice at constant velocity. The sheared DNA	
was blunt end-repaired with T4 DNA polymerase and T4	

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
Matches	28;	Conservative	0;	Mismatches	14;	Indels
						Gaps
						0
OY	2068	AATCGTTATAGCTTTAAAAATATATCCTGACGACCTTTTACATT	2109			
Db	4	AATCGCTTTTAATTTAAAAATATATTTGCTTATTTATTTATT	45			
LOCUS	BH221751	50 bp	DNA	linear	GSS	08-NOV-2001
DEFINITION	1006103B04.2EL_Y1	1006	-	RescueMu Grid G	zea mays	genomic, DNA
ACCESSION	BH221751					
VERSION	BH221751.1	GI:16816010				
KEYWORDS	GSS.					
SOURCE	Zea mays.					
ORGANISM	Zea mays					
	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC					
	clade; Panicoidae; Andropogoneae; Zea.					
	1 (bases 1 to 50)					
	Walbot, V.					
REFERENCE	Maize genomic sequences found using engineered RescueMu transposon					
AUTHORS	Unpublished (2001)					
TITLE	Contact: Walbot V					
JOURNAL	Department of Biological Sciences					
COMMENT	Stanford University					
	855 California Ave, Palo Alto, CA 94304, USA					
	Tel: 650 723 2227					
	Fax: 650 725 8221					
	Email: walbot@stanford.edu					
	Possible ligation site of ends cut by 2 different endonucleases.					
	Reverse complemented post-ligation sequence from source sequence.					
	Plate: 1006103 column: 37					
	Class: transposon-tagged.					
	Location/Qualifiers					
	1..50					
FEATURES	Source					
	/organism="Zea mays"					
	/cultivar="mixed background W23/A188/B73"					
	/db_xref="taxon:4577"					
	/clone_lib="1006 - RescueMu Grid G"					
	/tissue_type="leaf"					
	/dev_stage="adult"					
	/lab_host="DH10B"					
	/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."					



BASE COUNT 12 a 15 c 18 g 5 t  
ORIGIN

Query Match 0.8%; Score 19.6; DB 17; Length 50;  
Best Local Similarity 66.7%; Pred. No. 4.2e+06;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1884 AGGACCTTGGAGAGCAGGAGGACAGTGTAGGACAGGAGAGAAC 1925  
DB 9 AGCACCAGAGCCGAGCCAGTGCAGTGGGGAGTGTAGATC 50

Search completed: November 11, 2002, 02:35:09  
Job time : 2968 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic : nucleic search, using sw model

Run on: November 10, 2002, 23:22:02 ; Search time 5797 Seconds

(without alignments)  
11591.923 Million cell updates/sec

Title: US-09-659-860A-3

Sequence: 1 ggaagacgtgcagcccca.....gattaataatgtgtgtcctt 2309

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

GenBml: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pla: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	1.2	28	6	AR091202 Sequence
2	28	1.2	28	6	AR198237 Sequence
3	27.4	1.2	29	6	AR121773 Sequence
4	27.4	1.2	29	6	AR121774 Sequence
5	27	1.2	27	6	AR091106 Sequence
6	27	1.2	27	6	AR198141 Sequence
7	26	1.1	26	6	AR091105 Sequence
8	26	1.1	26	6	AR091201 Sequence
9	26	1.1	26	6	AR198140 Sequence
10	26	1.1	26	6	AR198236 Sequence
11	25.6	1.1	48	6	AX207739 Sequence
12	25.6	1.1	48	6	AX207745 Sequence
13	23.2	1.0	48	6	AS9018 Sequence
14	22.8	1.0	41	6	A66666 Sequence 11
15	22.8	1.0	49	6	AR139393 Sequence
16	22	1.0	50	6	AX159802 Sequence
17	21.8	0.9	37	6	A66667 Sequence 12
18	21.8	0.9	46	6	AS9017 Sequence 5
19	21.8	0.9	47	10	S82867 Apod-apol1p
20	21.8	0.9	49	6	AR207719 Sequence
21	21.6	0.9	49	6	AS9014 Sequence 2
22	21.4	0.9	45	6	AR124897 Sequence
23	21.4	0.9	48	6	AR134560 Sequence
24	21.2	0.9	47	6	AX094703 Sequence
25	21.2	0.9	48	6	AR153148 Sequence
26	21.2	0.9	48	6	AR210944 Sequence
27	21	0.9	45	6	AS9013 Sequence 1
28	21	0.9	48	12	SYNSYAPL4
29	21	0.9	50	6	AX159047 Sequence
30	20.8	0.9	43	6	AX484538 Sequence
31	20.8	0.9	49	6	A46759 Sequence 1
32	20.8	0.9	49	6	189340 Sequence 1
33	20.8	0.9	50	6	AX165053 Sequence
34	20.6	0.9	41	6	AR139408 Sequence
35	20.6	0.9	45	6	AR139392 Sequence
36	20.6	0.9	50	6	AX162670 Sequence
37	20.4	0.9	50	6	AX093098 Sequence
38	20.4	0.9	50	6	AX158156 Sequence
39	20.2	0.9	46	10	MMU242789 Mus muscu
40	20.2	0.9	50	6	AX161234 Sequence
41	20.2	0.9	50	6	AX162672 Sequence
42	20.2	0.9	50	6	AX162674 Sequence
43	20.2	0.9	50	6	E22339 DNA encodin
44	20.2	0.9	50	6	E22344 DNA encodin
45	20	0.9	36	6	AR084536 Sequence
46	20	0.9	38	6	AX361209 Sequence
47	20	0.9	39	6	A07129 Nucleotide
48	20	0.9	46	6	E03833 DNA encodin
49	20	0.9	46	6	AR059781 Sequence
50	19.8	0.9	50	6	E60006 Ceramide-bl
51	19.8	0.9	46	6	A98768 Sequence 1
52	19.8	0.9	47	6	AR166259 Sequence
53	19.8	0.9	48	4	AB022055 Canis fam
54	19.8	0.9	50	6	AX160090 Sequence
55	19.6	0.8	33	6	A66668 Sequence 13
56	19.6	0.8	36	6	AX179244 Sequence
57	19.6	0.8	48	6	AX13844 Nucleotide
58	19.6	0.8	49	6	AR093223 Sequence
59	19.4	0.8	35	6	AX061277 Sequence
60	19.4	0.8	35	6	AX061339 Sequence
61	19.4	0.8	36	6	AX061340 Sequence
62	19.4	0.8	37	6	AX061341 Sequence
63	19.4	0.8	38	6	AX061342 Sequence
64	19.4	0.8	38	6	AX223107 Sequence
65	19.4	0.8	39	6	AX061343 Sequence

Pred. No. is the number of results predicted by chance to have a

C 66	19.4	0.8	40	6	AR050327	Sequence	C 139	18.6	0.8	42	6	AR013771	Sequence
C 67	19.4	0.8	40	6	AX061344	Sequence	C 140	18.6	0.8	50	6	AR032855	Sequence
C 68	19.4	0.8	41	6	AX061282	Sequence	C 141	18.6	0.8	50	6	AR032857	Sequence
C 69	19.4	0.8	42	6	AX061283	Sequence	C 142	18.6	0.8	50	6	AR032857	Sequence
C 70	19.4	0.8	44	6	AX061284	Sequence	C 143	18.6	0.8	50	6	AR029519	Sequence
C 71	19.4	0.8	44	6	AX061285	Sequence	C 144	18.6	0.8	50	6	AR029521	Sequence
C 72	19.4	0.8	45	6	AX061286	Sequence	C 145	18.6	0.8	50	6	AX190073	Sequence
C 73	19.4	0.8	46	6	AX061287	Sequence	C 146	18.6	0.8	50	6	I29595	Sequence
C 74	19.4	0.8	47	6	AR211861	Sequence	C 147	18.6	0.8	50	6	I29597	Sequence
C 75	19.2	0.8	24	6	AX443237	Sequence	C 148	18.6	0.8	50	6	I91269	Sequence
C 76	19.2	0.8	24	6	AX443240	Sequence	C 149	18.6	0.8	50	6	I91271	Sequence
C 77	19.2	0.8	24	6	AX443257	Sequence	C 150	18.6	0.8	50	10	MMU41960	Sequence
C 78	19.2	0.8	35	6	AX443260	Sequence	C 151	18.4	0.8	29	6	MMU41975	Sequence
C 79	19.2	0.8	35	6	E02802	Sequence	C 152	18.4	0.8	30	6	AX253564	Sequence
C 80	19.2	0.8	36	6	AR105684	Sequence	C 153	18.4	0.8	30	6	AX033189	Sequence
C 81	19.2	0.8	38	6	AX404666	Sequence	C 154	18.4	0.8	31	6	AX061335	Sequence
C 82	19.2	0.8	41	6	AR032234	Sequence	C 155	18.4	0.8	32	6	AX061337	Sequence
C 83	19.2	0.8	41	6	AR201284	Sequence	C 156	18.4	0.8	33	6	AX061337	Sequence
C 84	19.2	0.8	43	9	HUMX	Sequence	C 157	18.4	0.8	34	6	AX061338	Sequence
C 85	19.2	0.8	45	6	AR167881	Sequence	C 158	18.4	0.8	34	11	C75760	Sequence
C 86	19.2	0.8	45	6	AX019802	Sequence	C 159	18.4	0.8	36	9	HSTCARB15	Sequence
C 87	19.2	0.8	48	6	I90209	Sequence	C 160	18.4	0.8	37	6	AX061278	Sequence
C 88	19.2	0.8	49	6	AX099434	Sequence	C 161	18.4	0.8	38	6	AX061279	Sequence
C 89	19.2	0.8	49	6	AR148167	Sequence	C 162	18.4	0.8	38	6	AX273910	Sequence
C 90	19.2	0.8	38	6	AX220343	Sequence	C 163	18.4	0.8	39	6	AX061280	Sequence
C 91	19.2	0.8	40	6	AX184221	Sequence	C 164	18.4	0.8	40	6	AR160226	Sequence
C 92	19.2	0.8	41	6	AR109076	Sequence	C 165	18.4	0.8	40	6	AX061281	Sequence
C 93	19.2	0.8	41	6	AR200731	Sequence	C 166	18.4	0.8	43	6	I08287	Sequence
C 94	19.2	0.8	45	6	AR168699	Sequence	C 167	18.4	0.8	44	6	AX431444	Sequence
C 95	19.2	0.8	45	6	AX027155	Sequence	C 168	18.4	0.8	44	6	E41646	Sequence
C 96	19.2	0.8	45	6	ES2000	Promoter, r	C 169	18.4	0.8	45	9	HSAN010619	Sequence
C 97	19.2	0.8	46	5	ELBETA6	Sequence	C 170	18.4	0.8	48	4	PIGCFTRB	Sequence
C 98	19.2	0.8	46	6	AR163660	Sequence	C 171	18.4	0.8	49	10	MUSJHCD6	Sequence
C 99	19.2	0.8	46	6	AX259566	Sequence	C 172	18.4	0.8	50	6	A95454	Sequence
C 100	19.2	0.8	48	9	CALCFTRB	Sequence	C 173	18.4	0.8	50	6	AR177517	Sequence
C 101	19.2	0.8	49	6	AR178011	Sequence	C 174	18.4	0.8	50	6	AX147176	Sequence
C 102	19.2	0.8	49	6	AR178012	Sequence	C 175	18.4	0.8	50	6	AX156809	Sequence
C 103	19.2	0.8	50	6	A39830	Sequence	C 176	18.4	0.8	50	6	AX156811	Sequence
C 104	19.2	0.8	50	6	AR044011	Sequence	C 177	18.4	0.8	50	6	AX160546	Sequence
C 105	19.2	0.8	50	6	AX158333	Sequence	C 178	18.4	0.8	50	10	I17034	Sequence
C 106	19.2	0.8	50	6	AX162190	Sequence	C 179	18.4	0.8	50	10	MUSRR45SY	Sequence
C 107	19.2	0.8	50	6	AX162668	Sequence	C 180	18.2	0.8	32	6	A63879	Sequence
C 108	18.8	0.8	31	6	AX203790	Sequence	C 181	18.2	0.8	33	6	AR050566	Sequence
C 109	18.8	0.8	38	6	AR058162	Sequence	C 182	18.2	0.8	36	6	I24913	Sequence
C 110	18.8	0.8	38	6	AR115920	Sequence	C 183	18.2	0.8	38	6	AX273965	Sequence
C 111	18.8	0.8	42	6	AX268903	Sequence	C 184	18.2	0.8	39	6	I82408	Sequence
C 112	18.8	0.8	42	6	AX268907	Sequence	C 185	18.2	0.8	41	6	AR019012	Sequence
C 113	18.8	0.8	43	6	AX483425	Sequence	C 186	18.2	0.8	41	6	AR111609	Sequence
C 114	18.8	0.8	46	6	E26015	Sequence	C 187	18.2	0.8	41	6	AR147009	Sequence
C 115	18.8	0.8	46	6	I31437	Sequence	C 188	18.2	0.8	41	6	AR158235	Sequence
C 116	18.8	0.8	47	6	AX194723	Sequence	C 189	18.2	0.8	42	6	AX006460	Sequence
C 117	18.8	0.8	48	1	TIP37CG2	Sequence	C 190	18.2	0.8	43	6	AX067973	Sequence
C 118	18.8	0.8	48	6	AR032614	Sequence	C 191	18.2	0.8	43	6	AX483385	Sequence
C 119	18.8	0.8	48	6	AR209278	Sequence	C 192	18.2	0.8	44	6	AX484515	Sequence
C 120	18.8	0.8	48	6	I29354	Sequence	C 193	18.2	0.8	44	6	AX050336	Sequence
C 121	18.8	0.8	48	6	I91028	Sequence	C 194	18.2	0.8	45	6	AR146542	Sequence
C 122	18.8	0.8	50	6	A25699	Sequence	C 195	18.2	0.8	48	6	AR202763	Sequence
C 123	18.8	0.8	50	6	AR051358	Sequence	C 196	18.2	0.8	48	9	S79501	Sequence
C 124	18.8	0.8	50	6	AR059787	Sequence	C 197	18.2	0.8	49	11	G73668	Sequence
C 125	18.8	0.8	50	6	AX158156	Sequence	C 198	18.2	0.8	50	6	AX158915	Sequence
C 126	18.8	0.8	50	6	AX162044	Sequence	C 199	18.2	0.8	50	6	AX160612	Sequence
C 127	18.8	0.8	50	6	AX196671	Sequence	C 200	18.2	0.8	50	6	AX175389	Sequence
C 128	18.8	0.8	50	6	AX342857	Sequence	C 201	18.2	0.8	50	6	AX190290	Sequence
C 129	18.8	0.8	50	6	E22340	Sequence	C 202	18.2	0.8	50	6	AX204199	Sequence
C 130	18.8	0.8	50	6	E22343	Sequence	C 203	18.2	0.8	50	6	AX204199	Sequence
C 131	18.6	0.8	29	6	AX046883	Sequence	C 204	18.2	0.8	34	6	AX406573	Sequence
C 132	18.6	0.8	35	6	E10813	Sequence	C 205	18.2	0.8	35	6	AR071839	Sequence
C 133	18.6	0.8	39	6	AR202194	Sequence	C 206	18.2	0.8	35	6	AR112579	Sequence
C 134	18.6	0.8	40	6	AR082637	Sequence	C 207	18.2	0.8	35	6	I74774	Sequence
C 135	18.6	0.8	40	6	I13193	Sequence	C 208	18.2	0.8	36	6	AR009886	Sequence
C 136	18.6	0.8	41	6	AR139391	Sequence	C 209	18.2	0.8	36	6	AR023668	Sequence
C 137	18.6	0.8	42	1	CTRB3AOMP3	Sequence	C 210	18.2	0.8	38	6	A73296	Sequence
C 138	18.6	0.8	42	1	CTRB3AOMP3	Sequence	C 211	18.2	0.8	38	6	AR061033	Sequence

C 212	18	0.8	38	6	AR161666	Sequence	C 285	17.8	0.8	48	6	I29323	I29323 Sequence 19
C 213	18	0.8	38	6	AX220323	Sequence	C 286	17.8	0.8	48	6	I90997	I90997 Sequence 19
C 214	18	0.8	42	6	AR220323	Sequence	C 287	17.8	0.8	49	6	AR023953	AR023953 Sequence
C 215	18	0.8	42	6	A13916	Nucleotide	C 288	17.8	0.8	49	6	AR205523	AR205523 Sequence
C 216	18	0.8	42	6	AR05061	Sequence	C 289	17.8	0.8	49	6	AX076533	AX076533 Sequence
C 217	18	0.8	42	6	AR060877	Sequence	C 290	17.8	0.8	49	6	AX076540	AX076540 Sequence
C 218	18	0.8	42	6	AR110811	Sequence	C 291	17.8	0.8	49	6	I15454	I15454 Sequence 32
C 219	18	0.8	42	6	I18290	Sequence	C 292	17.8	0.8	49	10	MUSIGHSWIT	M26302 Mus musculus
C 220	18	0.8	42	6	I24503	Sequence	C 293	17.8	0.8	50	6	AX147188	AX147188 Sequence
C 221	18	0.8	42	6	I28897	Sequence	C 294	17.8	0.8	50	10	MTEFAM13	U71389 Mus musculus
C 222	18	0.8	42	6	I33035	Sequence	C 295	17.8	0.8	50	12	SYN17XORE	K00455 chimeric pl
C 223	18	0.8	42	6	I79631	Sequence	C 296	17.6	0.8	24	6	AR202878	AR202878 Sequence
C 224	18	0.8	43	6	AR011922	Sequence	C 297	17.6	0.8	25	6	AX050440	AX050440 Sequence
C 225	18	0.8	43	6	AR017793	Sequence	C 298	17.6	0.8	25	6	AX076641	AX076641 Sequence
C 226	18	0.8	43	6	AR077198	Sequence	C 299	17.6	0.8	26	6	AX116990	AX116990 Sequence
C 227	18	0.8	43	6	AX394955	Sequence	C 300	17.6	0.8	28	6	AR094102	AR094102 Sequence
C 228	18	0.8	43	6	AX483555	Sequence	C 301	17.6	0.8	28	6	BD005768	BD005768 Therapeut
C 229	18	0.8	43	6	E38119	DNA elongat	C 302	17.6	0.8	29	6	A66669	A66669 Sequence 14
C 230	18	0.8	45	6	I55013	Sequence	C 303	17.6	0.8	34	6	AX358614	AX358614 Sequence
C 231	18	0.8	45	6	I55014	Sequence	C 304	17.6	0.8	35	6	A18124	A18124 Oligomer de
C 232	18	0.8	46	17	HSMC43F06	Sequence	C 305	17.6	0.8	35	6	I13227	I13227 Sequence 56
C 233	18	0.8	46	17	I77068	Sequence	C 306	17.6	0.8	36	6	AX467364	AX467364 Sequence
C 234	18	0.8	48	6	A76112	Sequence	C 307	17.6	0.8	36	6	I33839	I33839 Sequence 33
C 235	18	0.8	50	6	AX108703	Sequence	C 308	17.6	0.8	36	6	A45968	A45968 Sequence 15
C 236	18	0.8	50	6	AX157060	Sequence	C 309	17.6	0.8	38	6	AR048227	AR048227 Sequence
C 237	18	0.8	50	6	AX157272	Sequence	C 310	17.6	0.8	38	6	AX220262	AX220262 Sequence
C 238	18	0.8	50	6	AX158917	Sequence	C 311	17.6	0.8	38	6	AX220293	AX220293 Sequence
C 239	18	0.8	50	14	S44879	(5' end of A	C 312	17.6	0.8	38	6	AX220414	AX220414 Sequence
C 240	17.8	0.8	30	6	AR028268	Sequence	C 313	17.6	0.8	38	6	AX220459	AX220459 Sequence
C 241	17.8	0.8	30	6	AR028269	Sequence	C 314	17.6	0.8	38	6	AX228668	AX228668 Sequence
C 242	17.8	0.8	30	6	AR138672	Sequence	C 315	17.6	0.8	39	6	A66657	A66657 Sequence 2
C 243	17.8	0.8	31	6	A69294	Sequence	C 316	17.6	0.8	39	6	I42458	I42458 Sequence 7
C 244	17.8	0.8	31	6	A71971	Sequence	C 317	17.6	0.8	39	10	MUSBMP241	D45010 Mouse gene
C 245	17.8	0.8	31	6	AR147159	Sequence	C 318	17.6	0.8	40	6	AR206821	AR206821 Sequence
C 246	17.8	0.8	31	6	BD009847	Sequence	C 319	17.6	0.8	40	6	AR206823	AR206823 Sequence
C 247	17.8	0.8	32	3	SUPUR7AH	Sequence	C 320	17.6	0.8	40	6	AX001534	AX001534 Sequence
C 248	17.8	0.8	33	6	A47286	Sequence	C 321	17.6	0.8	40	6	AX001546	AX001546 Sequence
C 249	17.8	0.8	36	6	AR053365	Sequence	C 322	17.6	0.8	40	6	AX026106	AX026106 Sequence
C 250	17.8	0.8	36	6	AR131089	Sequence	C 323	17.6	0.8	40	6	AX026114	AX026114 Sequence
C 251	17.8	0.8	37	6	AR123484	Sequence	C 324	17.6	0.8	40	6	AX456321	AX456321 Sequence
C 252	17.8	0.8	38	6	A20219	Oligonucleo	C 325	17.6	0.8	40	6	I06599	I06599 Sequence 4
C 253	17.8	0.8	38	6	AR046020	Sequence	C 326	17.6	0.8	41	6	AR003335	AR003335 Sequence
C 254	17.8	0.8	38	6	AR047097	Sequence	C 327	17.6	0.8	41	6	AX078135	AX078135 Sequence
C 255	17.8	0.8	38	6	AX425211	Sequence	C 328	17.6	0.8	41	6	AX343814	AX343814 Sequence
C 256	17.8	0.8	38	6	I53072	Sequence	C 329	17.6	0.8	41	6	AX343816	AX343816 Sequence
C 257	17.8	0.8	38	6	I54149	Sequence	C 330	17.6	0.8	42	6	AX167628	AX167628 Sequence
C 258	17.8	0.8	39	6	AR009907	Sequence	C 331	17.6	0.8	43	6	AX483529	AX483529 Sequence
C 259	17.8	0.8	39	6	AR110046	Sequence	C 332	17.6	0.8	43	6	AX484544	AX484544 Sequence
C 260	17.8	0.8	39	6	AX047843	Sequence	C 333	17.6	0.8	43	6	E21661	E21661 Spermato
C 261	17.8	0.8	39	6	BD008910	High leve	C 334	17.6	0.8	44	6	AX287944	AX287944 Sequence
C 262	17.8	0.8	39	10	MMBWAHRNA	Sequence	C 335	17.6	0.8	44	6	E03020	E03020 DNA encod
C 263	17.8	0.8	40	6	A33232	Synthetic p	C 336	17.6	0.8	45	6	A00699	A00699 Artificial
C 264	17.8	0.8	42	6	AX458217	Sequence	C 337	17.6	0.8	45	6	AR001115	AR001115 Sequence
C 265	17.8	0.8	42	6	AX458218	Sequence	C 338	17.6	0.8	45	6	AR061322	AR061322 Sequence
C 266	17.8	0.8	42	6	BD011209	Human tel	C 339	17.6	0.8	45	6	AR061367	AR061367 Sequence
C 267	17.8	0.8	42	6	E36958	Human telom	C 340	17.6	0.8	45	6	AR088049	AR088049 Sequence
C 268	17.8	0.8	43	6	AX484577	Sequence	C 341	17.6	0.8	45	6	AR108221	AR108221 Sequence
C 269	17.8	0.8	44	6	AX195512	Sequence	C 342	17.6	0.8	45	6	AR108266	AR108266 Sequence
C 270	17.8	0.8	45	6	AR026316	Sequence	C 343	17.6	0.8	45	6	AR148171	AR148171 Sequence
C 271	17.8	0.8	45	6	AR032580	Sequence	C 344	17.6	0.8	45	6	I00379	I00379 Sequence 1
C 272	17.8	0.8	45	6	AR199538	Sequence	C 345	17.6	0.8	45	6	I16178	I16178 Sequence 4
C 273	17.8	0.8	45	6	AR209244	Sequence	C 346	17.6	0.8	45	6	I16223	I16223 Sequence 49
C 274	17.8	0.8	45	6	AX239587	Sequence	C 347	17.6	0.8	45	6	I45552	I45552 Sequence 1
C 275	17.8	0.8	45	6	I29320	Sequence	C 348	17.6	0.8	45	6	I45561	I45561 Sequence 10
C 276	17.8	0.8	45	6	I29394	Sequence	C 349	17.6	0.8	45	6	I66664	I66664 Sequence 4
C 277	17.8	0.8	46	6	I75984	Sequence	C 350	17.6	0.8	45	6	I66709	I66709 Sequence 49
C 278	17.8	0.8	47	6	AR100692	Sequence	C 351	17.6	0.8	45	6	I84758	I84758 Sequence 4
C 279	17.8	0.8	47	6	AR211840	Sequence	C 352	17.6	0.8	45	6	I84603	I84603 Sequence 49
C 280	17.8	0.8	47	9	S75517	Ig S mu/S e	C 353	17.6	0.8	46	6	AX398263	AX398263 Sequence
C 281	17.8	0.8	48	4	BOVCFTRA	Sequence	C 354	17.6	0.8	46	6	A76303	A76303 Sequence 9
C 282	17.8	0.8	48	4	SHPCFTRA	Sequence	C 355	17.6	0.8	48	6	AR211823	AR211823 Sequence
C 283	17.8	0.8	48	6	AR032583	Sequence	C 356	17.6	0.8	48	6	AX304314	AX304314 Sequence
C 284	17.8	0.8	48	6	AR209247	Sequence	C 357	17.6	0.8	48	10	MUSNOPI506	L41517 Mus musculu

C 358	17.6	0.8	49	6	124205	124205 Sequence 27	431	17.4	0.8	50	6	BD007536	BD007536 Novel con
C 359	17.6	0.8	50	6	AR032859	AR032859 Sequence	432	17.4	0.8	50	9	AF057509	AF057509 Homo sapi
C 360	17.6	0.8	50	6	AR074567	AR074567 Sequence	433	17.2	0.7	24	6	AX443293	AX443293 Sequence
C 361	17.6	0.8	50	6	AR157447	AR157447 Sequence	434	17.2	0.7	27	6	AR029611	AR029611 Sequence
C 362	17.6	0.8	50	6	AR209523	AR209523 Sequence	435	17.2	0.7	27	6	AX317201	AX317201 Sequence
C 363	17.6	0.8	50	6	AX160088	AX160088 Sequence	436	17.2	0.7	29	6	A90854	A90854 Sequence
C 364	17.6	0.8	50	6	AX160212	AX160212 Sequence	437	17.2	0.7	29	6	AX464640	AX464640 Sequence
C 365	17.6	0.8	50	6	AX160924	AX160924 Sequence	438	17.2	0.7	30	6	AX118403	AX118403 Sequence
C 366	17.6	0.8	50	6	AX161238	AX161238 Sequence	439	17.2	0.7	30	6	E41653	E41653 Antibody ag
C 367	17.6	0.8	50	6	AX199542	AX199542 Sequence	440	17.2	0.7	31	6	A45758	A45758 Sequence 15
C 368	17.6	0.8	50	6	AX233396	AX233396 Sequence	441	17.2	0.7	31	6	A92703	A92703 Sequence 16
C 369	17.6	0.8	50	6	AX441060	AX441060 Sequence	442	17.2	0.7	31	6	AR176183	AR176183 Sequence
C 370	17.6	0.8	50	6	AX485733	AX485733 Sequence	443	17.2	0.7	31	6	AX076626	AX076626 Sequence
C 371	17.6	0.8	50	6	I29599	I29599 Sequence 47	444	17.2	0.7	31	6	AX076627	AX076627 Sequence
C 372	17.6	0.8	50	6	I91273	I91273 Sequence 47	445	17.2	0.7	31	6	AX082570	AX082570 Sequence
C 373	17.6	0.8	50	9	YSCFVID1	M24990 S.cerevisia	446	17.2	0.7	33	6	AR099242	AR099242 Sequence
C 374	17.6	0.8	50	9	HSTFEI14	X84968 H.sapiens t	447	17.2	0.7	35	6	AX369210	AX369210 Sequence
C 375	17.6	0.8	50	10	MMU41944	U41944 Mus musculu	448	17.2	0.7	37	6	AR210413	AR210413 Sequence
C 376	17.6	0.8	50	10	MMU41963	U41963 Mus musculu	449	17.2	0.7	37	6	AX147670	AX147670 Sequence
C 377	17.4	0.8	29	6	AX042792	AX042792 Sequence	450	17.2	0.7	37	6	AX16090	AX16090 Sequence
C 378	17.4	0.8	29	6	AX004697	AX004697 Sequence	451	17.2	0.7	37	6	E37284	E37284 Process for
C 379	17.4	0.8	29	6	AX236872	AX236872 Sequence	452	17.2	0.7	37	6	E37495	E37495 Process for
C 380	17.4	0.8	29	6	AX236886	AX236886 Sequence	453	17.2	0.7	37	6	E48955	E48955 Process for
C 381	17.4	0.8	29	6	AX239782	AX239782 Sequence	454	17.2	0.7	37	6	I92391	I92391 Sequence 43
C 382	17.4	0.8	30	6	AR093240	AR093240 Sequence	455	17.2	0.7	38	1	ASNTFRS2	X05594 Anabaena n1
C 383	17.4	0.8	30	6	AR101053	AR101053 Sequence	456	17.2	0.7	38	6	AR147037	AR147037 Sequence
C 384	17.4	0.8	30	6	AX057818	AX057818 Sequence	457	17.2	0.7	38	6	AX220372	AX220372 Sequence
C 385	17.4	0.8	35	6	AX039040	AX039040 Sequence	458	17.2	0.7	38	6	AX425390	AX425390 Sequence
C 386	17.4	0.8	36	6	AR050709	AR050709 Sequence	459	17.2	0.7	39	6	A06487	A06487 Nucleotide
C 387	17.4	0.8	36	6	AR093346	AR093346 Sequence	460	17.2	0.7	39	6	A06488	A06488 reverse com
C 388	17.4	0.8	36	6	AR147719	AR147719 Sequence	461	17.2	0.7	39	6	AR016773	AR016773 Sequence
C 389	17.4	0.8	36	6	AR159741	AR159741 Sequence	462	17.2	0.7	39	6	AR081956	AR081956 Sequence
C 390	17.4	0.8	36	6	AR160433	AR160433 Sequence	463	17.2	0.7	40	6	AR034248	AR034248 Sequence
C 391	17.4	0.8	36	6	AR202389	AR202389 Sequence	464	17.2	0.7	40	6	AR172313	AR172313 Sequence
C 392	17.4	0.8	38	6	AX220342	AX220342 Sequence	465	17.2	0.7	40	6	AR172314	AR172314 Sequence
C 393	17.4	0.8	38	6	AX220360	AX220360 Sequence	466	17.2	0.7	40	6	AX078179	AX078179 Sequence
C 394	17.4	0.8	38	6	AX220514	AX220514 Sequence	467	17.2	0.7	41	6	E58475	E58475 Process for
C 395	17.4	0.8	38	6	AX223130	AX223130 Sequence	468	17.2	0.7	41	6	A32270	A32270 mutagenic P
C 396	17.4	0.8	38	6	AX273972	AX273972 Sequence	469	17.2	0.7	41	6	AX078146	AX078146 Sequence
C 397	17.4	0.8	39	6	AX425408	AX425408 Sequence	470	17.2	0.7	41	6	152201	152201 Sequence 1
C 398	17.4	0.8	39	6	AX377747	AX377747 Sequence	471	17.2	0.7	42	6	AR031676	AR031676 Sequence
C 399	17.4	0.8	40	6	AR184397	AR184397 Sequence	472	17.2	0.7	42	6	AR075444	AR075444 Sequence
C 400	17.4	0.8	42	6	A43626	A43626 Sequence 16	473	17.2	0.7	42	6	AX027286	AX027286 Sequence
C 401	17.4	0.8	42	6	A84189	A84189 Sequence 14	474	17.2	0.7	42	6	AX181200	AX181200 Sequence
C 402	17.4	0.8	42	6	AR051094	AR051094 Sequence	475	17.2	0.7	42	6	190294	190294 Sequence 36
C 403	17.4	0.8	43	6	A04412	A04412 Oligonucleo	476	17.2	0.7	42	1	TRN45561	M19280 Transposon
C 404	17.4	0.8	43	6	AR200693	AR200693 Sequence	477	17.2	0.7	43	6	AX084432	AX084432 Sequence
C 405	17.4	0.8	44	6	A94092	A94092 Sequence 73	478	17.2	0.7	43	6	AX084544	AX084544 Sequence
C 406	17.4	0.8	44	6	AR077611	AR077611 Sequence	479	17.2	0.7	43	6	A30410	A30410 Sequence
C 407	17.4	0.8	44	6	AR183291	AR183291 Sequence	480	17.2	0.7	44	6	AX167841	AX167841 Sequence
C 408	17.4	0.8	44	6	AX011177	AX011177 Sequence	481	17.2	0.7	45	6	A45617	AX167842 Sequence
C 409	17.4	0.8	44	6	AX105035	AX105035 Sequence	482	17.2	0.7	45	6	A94953	A94953 Sequence 11
C 410	17.4	0.8	44	6	AX300148	AX300148 Sequence	483	17.2	0.7	45	6	AX061292	A94954 Sequence 39
C 411	17.4	0.8	44	9	I20743	I20743 Sequence 8	484	17.2	0.7	45	6	AR033074	AR033074 Sequence
C 412	17.4	0.8	44	9	S72295S1	S72295 Gp1A-Platel	485	17.2	0.7	45	6	AX061292	AX061292 Sequence
C 413	17.4	0.8	47	6	AR028906	AR028906 Sequence	486	17.2	0.7	45	6	AR147209	AR147209 Sequence
C 414	17.4	0.8	47	6	AR070123	AR070123 Sequence	487	17.2	0.7	45	6	AR202460	AR202460 Sequence
C 415	17.4	0.8	47	6	AR070311	AR070311 Sequence	488	17.2	0.7	46	6	AX076700	AX076700 Sequence
C 416	17.4	0.8	47	6	AR211466	AR211466 Sequence	489	17.2	0.7	46	6	AX076701	AX076701 Sequence
C 417	17.4	0.8	47	6	AX194757	AX194757 Sequence	490	17.2	0.7	46	6	AX076702	AX076702 Sequence
C 418	17.4	0.8	48	6	AX195039	AX195039 Sequence	491	17.2	0.7	46	6	AX080033	AX080033 Sequence
C 419	17.4	0.8	48	10	MUSCFITB	M75125 Mouse cystl	492	17.2	0.7	46	6	AX089634	AX089634 Sequence
C 420	17.4	0.8	50	6	A92072	A92072 Sequence 13	493	17.2	0.7	46	6	AX108725	AX108725 Sequence
C 421	17.4	0.8	50	6	A92073	A92073 Sequence 14	494	17.2	0.7	46	6	AX113385	AX113385 Sequence
C 422	17.4	0.8	50	6	AR148090	AR148090 Sequence	495	17.2	0.7	46	6	AX113385	AX113385 Sequence
C 423	17.4	0.8	50	6	AX160946	AX160946 Sequence	496	17.2	0.7	46	6	AX138254	AX138254 Sequence
C 424	17.4	0.8	50	6	AX161236	AX161236 Sequence	497	17.2	0.7	47	6	HIEGCG8	HIEGCG8
C 425	17.4	0.8	50	6	AX162368	AX162368 Sequence	498	17.2	0.7	48	1	A08375	A08375 Oligonucleo
C 426	17.4	0.8	50	6	AX164931	AX164931 Sequence	499	17.2	0.7	48	6		
C 427	17.4	0.8	50	6	AX233377	AX233377 Sequence	500	17.2	0.7	48	6		
C 428	17.4	0.8	50	6	AX316932	AX316932 Sequence	501	17.2	0.7	48	6		
C 429	17.4	0.8	50	6	AX403276	AX403276 Sequence	502	17.2	0.7	48	6		
C 430	17.4	0.8	50	6	BD007535	BD007535 Novel con	503	17.2	0.7	48	6		

504	17.2	0.7	48	6	150017	150017 Sequence 15	c 577	17	0.7	42	1	CTB24BOMP3	AF070273 Chlamydia
505	17.2	0.7	48	10	RNU34914	U94914 Rattus norv	c 578	17	0.7	42	1	CTB2AOMP3	AF070253 Chlamydia
506	17.2	0.7	49	6	AR070482	AR070482 Sequence	c 579	17	0.7	42	1	CTB2BOMP3	AF070261 Chlamydia
507	17.2	0.7	49	6	AX000861	AX000861 Sequence	c 580	17	0.7	42	1	CTB2COMP3	AF070265 Chlamydia
508	17.2	0.7	49	6	I20190	I20190 Sequence 5	c 581	17	0.7	42	1	CTB2DOMP3	AF070269 Chlamydia
509	17.2	0.7	49	6	I43038	I43038 Sequence 21	c 582	17	0.7	42	1	CTB2EOMP3	AF070281 Chlamydia
510	17.2	0.7	50	6	AR032732	AR032732 Sequence	c 583	17	0.7	42	1	CTB2FOMP3	AF070285 Chlamydia
511	17.2	0.7	50	6	AR032778	AR032778 Sequence	c 584	17	0.7	42	1	CTB4AOMP3	AF070293 Chlamydia
512	17.2	0.7	50	6	AR209396	AR209396 Sequence	c 585	17	0.7	42	1	CTB4BOMP3	AF070297 Chlamydia
513	17.2	0.7	50	6	AR209442	AR209442 Sequence	c 586	17	0.7	42	1	CTB4COMP3	AF070301 Chlamydia
514	17.2	0.7	50	6	AX160388	AX160388 Sequence	c 587	17	0.7	42	1	CTB4DOMP3	AF070305 Chlamydia
515	17.2	0.7	50	6	AX160663	AX160663 Sequence	c 588	17	0.7	42	1	CTB6MP3	AF070223 Chlamydia
516	17.2	0.7	50	6	AX164938	AX164938 Sequence	c 589	17	0.7	42	1	CTBREFBOMP3	AF070227 Chlamydia
517	17.2	0.7	50	6	AX164939	AX164939 Sequence	c 590	17	0.7	42	6	A12253	A12253 Nucleotide
518	17.2	0.7	50	6	AX330853	AX330853 Sequence	c 591	17	0.7	42	6	A12254	A12254 Nucleotide
519	17.2	0.7	50	6	I29472	I29472 Sequence 34	c 592	17	0.7	42	6	A22335	A22335 Primer O-5
520	17.2	0.7	50	6	I29518	I29518 Sequence 39	c 593	17	0.7	42	6	AR036048	AR036048 Sequence
521	17.2	0.7	50	6	I42242	I42242 Sequence 55	c 594	17	0.7	42	6	AR071819	AR071819 Sequence
522	17.2	0.7	50	6	I42243	I42243 Sequence 56	c 595	17	0.7	42	6	AR112559	AR112559 Sequence
523	17.2	0.7	50	6	I91146	I91146 Sequence 34	c 596	17	0.7	42	6	AR112635	AR112635 Sequence
524	17.2	0.7	50	6	I91192	I91192 Sequence 39	c 597	17	0.7	42	6	AX079214	AX079214 Sequence
525	17.2	0.7	50	9	AF057516	AF057516 Homo sapi	c 598	17	0.7	42	6	AX080047	AX080047 Sequence
526	17.2	0.7	50	10	MMU41965	U41965 Mus musculu	c 599	17	0.7	42	6	AX080057	AX080057 Sequence
527	17	0.7	30	6	AR084918	AR084918 Sequence	c 600	17	0.7	42	6	E12872	E12872 Primer 4/1
528	17	0.7	30	6	AR204083	AR204083 Sequence	c 601	17	0.7	42	6	E35712	E35712 Method for
529	17	0.7	30	6	AX024999	AX024999 Sequence	c 602	17	0.7	42	6	I14320	I14320 Sequence 18
530	17	0.7	30	6	AX282528	AX282528 Sequence	c 603	17	0.7	42	6	I85726	I85726 Sequence 75
531	17	0.7	30	6	E50447	E50447 Odoriferous	c 604	17	0.7	42	11	AL773259	AL773259 Arabidops
532	17	0.7	33	6	AR079765	AR079765 Sequence	c 605	17	0.7	43	6	A05113	A05113 Oligonucleo
533	17	0.7	33	6	AR081295	AR081295 Sequence	c 606	17	0.7	43	6	AX483499	AX483499 Sequence
534	17	0.7	33	6	AR170655	AR170655 Sequence	c 607	17	0.7	43	6	AX484397	AX484397 Sequence
535	17	0.7	34	6	AR012331	AR012331 Sequence	c 608	17	0.7	43	6	AX484537	AX484537 Sequence
536	17	0.7	34	6	AR012334	AR012334 Sequence	c 609	17	0.7	43	6	AX484545	AX484545 Sequence
537	17	0.7	34	6	AR111892	AR111892 Sequence	c 610	17	0.7	44	6	AR110224	AR110224 Sequence
538	17	0.7	34	6	AR142228	AR142228 Sequence	c 611	17	0.7	44	6	AR110237	AR110237 Sequence
539	17	0.7	35	6	AR095225	AR095225 Sequence	c 612	17	0.7	44	6	AR168983	AR168983 Sequence
540	17	0.7	35	6	AR125192	AR125192 Sequence	c 613	17	0.7	44	6	AR169996	AR169996 Sequence
541	17	0.7	35	6	I38829	I38829 Sequence 16	c 614	17	0.7	44	6	AR171792	AR171792 Sequence
542	17	0.7	36	6	AR033955	AR033955 Sequence	c 615	17	0.7	44	6	AR171805	AR171805 Sequence
543	17	0.7	36	6	AR175088	AR175088 Sequence	c 616	17	0.7	44	6	BD009017	BD009017 Promoter
544	17	0.7	36	6	AX032556	AX032556 Sequence	c 617	17	0.7	44	6	BD009030	BD009030 Promoter
545	17	0.7	36	6	AX236831	AX236831 Sequence	c 618	17	0.7	45	6	A05540	A05540 Oligonucleo
546	17	0.7	36	6	AX298175	AX298175 Sequence	c 619	17	0.7	45	6	AR09910	AR09910 Sequence 5
547	17	0.7	38	6	AR011526	AR011526 Sequence	c 620	17	0.7	45	6	AR001633	AR001633 Sequence
548	17	0.7	38	6	AX220255	AX220255 Sequence	c 621	17	0.7	45	6	AR066029	AR066029 Sequence
549	17	0.7	38	6	AX220349	AX220349 Sequence	c 622	17	0.7	45	6	AR120359	AR120359 Sequence
550	17	0.7	38	6	AX220350	AX220350 Sequence	c 623	17	0.7	45	6	AR149770	AR149770 Sequence
551	17	0.7	38	6	AX220358	AX220358 Sequence	c 624	17	0.7	45	6	AR205027	AR205027 Sequence
552	17	0.7	38	6	AX220431	AX220431 Sequence	c 625	17	0.7	45	6	AX027579	AX027579 Sequence
553	17	0.7	38	6	AX228647	AX228647 Sequence	c 626	17	0.7	45	6	AX027580	AX027580 Sequence
554	17	0.7	38	6	AX228667	AX228667 Sequence	c 627	17	0.7	45	6	AX074248	AX074248 Sequence
555	17	0.7	38	6	AX273554	AX273554 Sequence	c 628	17	0.7	45	6	AX082538	AX082538 Sequence
556	17	0.7	38	6	AX273891	AX273891 Sequence	c 629	17	0.7	45	6	AX370653	AX370653 Sequence
557	17	0.7	38	6	AX274016	AX274016 Sequence	c 630	17	0.7	45	6	AX377734	AX377734 Sequence
558	17	0.7	38	6	AX25412	AX25412 Sequence	c 631	17	0.7	45	6	AX477478	AX477478 Sequence
559	17	0.7	38	6	E11257	E11257 PCR primer	c 632	17	0.7	45	6	BD010483	BD010483 Agents fo
560	17	0.7	38	6	I18164	I18164 Sequence 40	c 633	17	0.7	45	6	I09090	I09090 Sequence 9
561	17	0.7	39	6	AR128128	AR128128 Sequence	c 634	17	0.7	45	6	I28424	I28424 Sequence 5
562	17	0.7	39	6	AR164496	AR164496 Sequence	c 635	17	0.7	45	10	RATMLV5	RATMLV5 Rat provira
563	17	0.7	39	6	AX081623	AX081623 Sequence	c 636	17	0.7	46	6	AR032675	AR032675 Sequence
564	17	0.7	39	6	AX374804	AX374804 Sequence	c 637	17	0.7	46	6	AR122347	AR122347 Sequence
565	17	0.7	39	6	AX461676	AX461676 Sequence	c 638	17	0.7	46	6	AR131221	AR131221 Sequence
566	17	0.7	39	9	HS010897	HS010897 Homo sapi	c 639	17	0.7	46	6	AR209339	AR209339 Sequence
567	17	0.7	40	6	AX035990	AX035990 Sequence	c 640	17	0.7	46	6	I29415	I29415 Sequence 28
568	17	0.7	41	6	AR182108	AR182108 Sequence	c 641	17	0.7	46	6	I91089	I91089 Sequence 28
569	17	0.7	41	6	I07162	I07162 Sequence 4	c 642	17	0.7	47	6	AR079493	AR079493 Sequence
570	17	0.7	42	1	AF178265S3	AF178265 Chlamydia	c 643	17	0.7	47	6	AR194747	AR194747 Sequence
571	17	0.7	42	1	AF178269S3	AF178271 Chlamydia	c 644	17	0.7	47	6	AX378277	AX378277 Sequence
572	17	0.7	42	1	AF178273S3	AF178275 Chlamydia	c 645	17	0.7	47	6	AX378506	AX378506 Sequence
573	17	0.7	42	1	CTB124AOMP3	AF070249 Chlamydia	c 646	17	0.7	48	6	A22117	A22117 Integrated
574	17	0.7	42	1	CTB12AOMP3	AF070245 Chlamydia	c 647	17	0.7	48	6	A22119	A22119 thrombin an
575	17	0.7	42	1	CTB1AOMP3	AF070241 Chlamydia	c 648	17	0.7	48	6	I45633	I45633 Sequence 21
576	17	0.7	42	1	CTB24AOMP3	AF070257 Chlamydia	c 649	17	0.7	48	6	I45633	I45633 Sequence 21

650	17	0.7	48	6	I45634	I45634 Sequence 23	723	16.8	0.7	36	6	AX000359	AX000359 Sequence
651	17	0.7	48	10	RNU34914	U34914 Rattus norv	C 724	16.8	0.7	36	6	AX469988	AX469988 Sequence
652	17	0.7	48	17	HSCHO6F06	X88550 H. sapiens D	C 725	16.8	0.7	36	6	I26097	I26097 Sequence 23
653	17	0.7	49	6	AB3844	AB3844 Sequence 3	C 726	16.8	0.7	36	6	I36091	I36091 Sequence 41
654	17	0.7	49	6	AR011234	AR011234 Sequence	C 727	16.8	0.7	37	6	AR139390	AR139390 Sequence
655	17	0.7	49	6	AR011235	AR011235 Sequence	C 728	16.8	0.7	37	6	AR047325	AR047325 Sequence
656	17	0.7	49	6	AR093225	AR093225 Sequence	C 729	16.8	0.7	38	6	AX219023	AX219023 Sequence
657	17	0.7	49	6	AR146538	AR146538 Sequence	C 730	16.8	0.7	38	6	AX220295	AX220295 Sequence
658	17	0.7	49	6	I17872	I17872 Sequence 10	C 731	16.8	0.7	38	6	AX273980	AX273980 Sequence
659	17	0.7	49	6	I17873	I17873 Sequence 10	C 732	16.8	0.7	38	6	AX425304	AX425304 Sequence
660	17	0.7	49	6	I42247	I42247 Sequence 60	C 733	16.8	0.7	38	6	AX425357	AX425357 Sequence
661	17	0.7	50	5	XELRGT2A	M13247 X. borealis	C 734	16.8	0.7	38	6	AX425473	AX425473 Sequence
662	17	0.7	50	6	A02843	A02843 Artificial	C 735	16.8	0.7	38	6	BD012638	BD012638 Human cyt
663	17	0.7	50	6	A12059	A12059 Oligonucleo	C 736	16.8	0.7	38	6	I54377	I54377 Sequence 21
664	17	0.7	50	6	A25699	A25699 MOVHLINK3 p	C 737	16.8	0.7	38	23	BD008206	BD008206 Human cyt
665	17	0.7	50	6	AR032771	AR032771 Sequence	C 738	16.8	0.7	39	6	AR001557	AR001557 Sequence
666	17	0.7	50	6	AR032856	AR032856 Sequence	C 739	16.8	0.7	39	6	AR093715	AR093715 Sequence
667	17	0.7	50	6	AR051358	AR051358 Sequence	C 740	16.8	0.7	39	6	AR139643	AR139643 Sequence
668	17	0.7	50	6	AR209435	AR209435 Sequence	C 741	16.8	0.7	39	6	AR165977	AR165977 Sequence
669	17	0.7	50	6	AR209520	AR209520 Sequence	C 742	16.8	0.7	39	6	AR182871	AR182871 Sequence
670	17	0.7	50	6	AX079226	AX079226 Sequence	C 743	16.8	0.7	39	6	AX000902	AX000902 Sequence
671	17	0.7	50	6	AX080068	AX080068 Sequence	C 744	16.8	0.7	39	6	E11258	E11258 PCR primer
672	17	0.7	50	6	AX127337	AX127337 Sequence	C 745	16.8	0.7	39	6	E60089	E60089 Endonucleas
673	17	0.7	50	6	AX162041	AX162041 Sequence	C 746	16.8	0.7	40	6	A65366	A65366 Sequence 2
674	17	0.7	50	6	AX162710	AX162710 Sequence	C 747	16.8	0.7	40	6	AR100922	AR100922 Sequence
675	17	0.7	50	6	AX190222	AX190222 Sequence	C 748	16.8	0.7	40	6	AX136807	AX136807 Sequence
676	17	0.7	50	6	AX199704	AX199704 Sequence	C 749	16.8	0.7	40	6	AX456219	AX456219 Sequence
677	17	0.7	50	6	E50448	E50448 Odoriferous	C 750	16.8	0.7	40	6	E11812	E11812 Synthetic r
678	17	0.7	50	6	I29511	I29511 Sequence 38	C 751	16.8	0.7	40	6	E11812	E11812 Synthetic r
679	17	0.7	50	6	I29596	I29596 Sequence 46	C 752	16.8	0.7	40	6	E64594	E64594 Immobilizat
680	17	0.7	50	6	I91185	I91185 Sequence 38	C 753	16.8	0.7	40	6	E64600	E64600 Immobilizat
681	17	0.7	50	6	I91270	I91270 Sequence 46	C 754	16.8	0.7	40	6	AX059989	AX059989 Sequence
682	17	0.7	50	6	I91270	I91270 Sequence 46	C 755	16.8	0.7	41	6	AX128530	AX128530 Sequence
683	17	0.7	50	10	AF357428	AF357428 Mus muscu	C 756	16.8	0.7	41	6	AX128530	AX128530 Sequence
684	16.8	0.7	25	6	AX139465	AX139465 Sequence	C 757	16.8	0.7	41	6	AX128531	AX128531 Sequence
685	16.8	0.7	28	6	AX033186	AX033186 Sequence	C 758	16.8	0.7	41	6	AX303601	AX303601 Sequence
686	16.8	0.7	30	6	AR028237	AR028237 Sequence	C 759	16.8	0.7	41	6	AX327077	AX327077 Sequence
687	16.8	0.7	30	6	AR138640	AR138640 Sequence	C 760	16.8	0.7	41	6	I12934	I12934 Sequence 14
688	16.8	0.7	31	6	AR7137	AR7137 Sequence 47	C 761	16.8	0.7	41	6	I12934	I12934 Sequence 15
689	16.8	0.7	31	6	AR053308	AR053308 Sequence	C 762	16.8	0.7	42	6	AR82218	AR82218 Sequence 39
690	16.8	0.7	31	6	AR157880	AR157880 Sequence	C 763	16.8	0.7	42	6	AR061602	AR061602 Sequence
691	16.8	0.7	31	6	AR206391	AR206391 Sequence	C 764	16.8	0.7	42	6	AR108501	AR108501 Sequence
692	16.8	0.7	31	6	AX247993	AX247993 Sequence	C 765	16.8	0.7	42	6	BD007247	BD007247 Novel flt
693	16.8	0.7	31	6	E14250	E14250 PCR primer.	C 766	16.8	0.7	42	6	I16458	I16458 Sequence 28
694	16.8	0.7	31	6	I40527	I40527 PCR primer.	C 767	16.8	0.7	42	6	I66944	I66944 Sequence 28
695	16.8	0.7	32	6	AR7073	AR7073 Sequence 1	C 768	16.8	0.7	42	6	I85038	I85038 Sequence 28
696	16.8	0.7	32	6	AR7165	AR7165 Sequence 25	C 769	16.8	0.7	42	10	MMVA2JLJN	MMVA2JLJN
697	16.8	0.7	32	6	AX003993	AX003993 Sequence	C 770	16.8	0.7	43	6	A42692	A42692 Sequence 24
698	16.8	0.7	33	6	AR138756	AR138756 Sequence	C 771	16.8	0.7	43	6	A46250	A46250 Sequence 13
699	16.8	0.7	33	6	AR176894	AR176894 Sequence	C 772	16.8	0.7	43	6	AR006749	AR006749 Sequence
700	16.8	0.7	33	6	AR183645	AR183645 Sequence	C 773	16.8	0.7	43	6	AR032025	AR032025 Sequence
701	16.8	0.7	33	6	AX428309	AX428309 Sequence	C 774	16.8	0.7	43	6	AR038521	AR038521 Sequence
702	16.8	0.7	33	6	I34695	I34695 Sequence 1	C 775	16.8	0.7	43	6	AR050868	AR050868 Sequence
703	16.8	0.7	34	6	AR004913	AR004913 Sequence	C 776	16.8	0.7	43	6	AR170480	AR170480 Sequence
704	16.8	0.7	34	6	AR020595	AR020595 Sequence	C 777	16.8	0.7	43	6	AX483393	AX483393 Sequence
705	16.8	0.7	34	6	E11259	E11259 PCR primer	C 778	16.8	0.7	43	6	AX483512	AX483512 Sequence
706	16.8	0.7	35	6	AR051303	AR051303 Sequence	C 779	16.8	0.7	43	6	AX484504	AX484504 Sequence
707	16.8	0.7	35	6	AX076480	AX076480 Sequence	C 780	16.8	0.7	43	6	E05892	E05892 Sequence
708	16.8	0.7	35	6	I16951	I16951 Sequence 20	C 781	16.8	0.7	43	6	E07925	E07925 Synthetic D
709	16.8	0.7	35	6	I45745	I45745 Sequence 20	C 782	16.8	0.7	43	6	I20189	I20189 Sequence 4
710	16.8	0.7	35	11	C75916	C75916 Homo sapien	C 783	16.8	0.7	43	6	I87198	I87198 Sequence 24
711	16.8	0.7	36	6	AB7134	AB7134 Sequence 44	C 784	16.8	0.7	44	6	A42693	A42693 Sequence 25
712	16.8	0.7	36	6	AB7179	AB7179 Sequence 14	C 785	16.8	0.7	44	6	AR009880	AR009880 Sequence
713	16.8	0.7	36	6	AR044451	AR044451 Sequence	C 786	16.8	0.7	44	6	AX202534	AX202534 Sequence
714	16.8	0.7	36	6	AR058944	AR058944 Sequence	C 787	16.8	0.7	44	6	I65727	I65727 Sequence 87
715	16.8	0.7	36	6	AR105218	AR105218 Sequence	C 788	16.8	0.7	44	6	I67959	I67959 Sequence 87
716	16.8	0.7	36	6	AR119139	AR119139 Sequence	C 789	16.8	0.7	44	6	I87199	I87199 Sequence 25
717	16.8	0.7	36	6	AR123510	AR123510 Sequence	C 790	16.8	0.7	44	9	HS2421937	HS2421937 Homo sapi
718	16.8	0.7	36	6	AR138163	AR138163 Sequence	C 791	16.8	0.7	45	6	A05131	A05131 Oligonucleo
719	16.8	0.7	36	6	AR176724	AR176724 Sequence	C 792	16.8	0.7	45	6	A38867	A38867 Sequence 21
720	16.8	0.7	36	6	AR198295	AR198295 Sequence	C 793	16.8	0.7	45	6	A73055	A73055 Sequence 31
721	16.8	0.7	36	6	AR200507	AR200507 Sequence	C 794	16.8	0.7	45	6	A73147	A73147 Sequence 31
722	16.8	0.7	36	6	AR206388	AR206388 Sequence	C 795	16.8	0.7	45	6	AR001556	AR001556 Sequence



796	16.8	0.7	45	6	AR044290	Sequence	AR044290	Sequence	869	16.6	0.7	35	6	AX082923	Sequence	AX082923	Sequence
C 797	16.8	0.7	45	6	AR126951	Sequence	AR126951	Sequence	C 870	16.6	0.7	35	6	AX082950	Sequence	AX082950	Sequence
C 798	16.8	0.7	45	6	AR145065	Sequence	AR145065	Sequence	C 871	16.6	0.7	35	6	AX146697	Sequence	AX146697	Sequence
C 799	16.8	0.7	45	6	AR174696	Sequence	AR174696	Sequence	C 872	16.6	0.7	35	6	AX199055	Sequence	AX199055	Sequence
C 800	16.8	0.7	45	6	AX146974	Sequence	AX146974	Sequence	C 873	16.6	0.7	35	6	AX329316	Sequence	AX329316	Sequence
C 801	16.8	0.7	45	6	135930	Sequence	135930	Sequence	C 874	16.6	0.7	35	6	AX468238	Sequence	AX468238	Sequence
C 802	16.8	0.7	45	9	HD013COL23	Sequence	HD013COL23	Sequence	C 875	16.6	0.7	35	6	E08875	Sequence	E08875	Sequence
C 803	16.8	0.7	45	9	AR008149	Sequence	AR008149	Sequence	C 876	16.6	0.7	35	11	C75873	Sequence	C75873	Sequence
C 804	16.8	0.7	46	6	AX225288	Sequence	AX225288	Sequence	C 877	16.6	0.7	35	11	C75873	Sequence	C75873	Sequence
C 805	16.8	0.7	46	6	AX225301	Sequence	AX225301	Sequence	C 878	16.6	0.7	36	6	A27217	Sequence	A27217	Sequence
C 806	16.8	0.7	46	6	AX473358	Sequence	AX473358	Sequence	C 879	16.6	0.7	36	6	A27217	Sequence	A27217	Sequence
C 807	16.8	0.7	47	6	AR079494	Sequence	AR079494	Sequence	C 880	16.6	0.7	36	6	AR028705	Sequence	AR028705	Sequence
C 808	16.8	0.7	47	6	AR110499	Sequence	AR110499	Sequence	C 881	16.6	0.7	36	6	AR053365	Sequence	AR053365	Sequence
C 809	16.8	0.7	47	6	AR110500	Sequence	AR110500	Sequence	C 882	16.6	0.7	36	6	AR131089	Sequence	AR131089	Sequence
C 810	16.8	0.7	47	6	AR137052	Sequence	AR137052	Sequence	C 883	16.6	0.7	36	6	AX417156	Sequence	AX417156	Sequence
C 811	16.8	0.7	47	6	AR137053	Sequence	AR137053	Sequence	C 884	16.6	0.7	37	6	AR069344	Sequence	AR069344	Sequence
C 812	16.8	0.7	47	6	AX194679	Sequence	AX194679	Sequence	C 885	16.6	0.7	37	6	AX183678	Sequence	AX183678	Sequence
C 813	16.8	0.7	47	6	AX194962	Sequence	AX194962	Sequence	C 886	16.6	0.7	37	6	164561	Sequence	164561	Sequence
C 814	16.8	0.7	47	6	AX378281	Sequence	AX378281	Sequence	C 887	16.6	0.7	38	6	AR170829	Sequence	AR170829	Sequence
C 815	16.8	0.7	47	6	AX452868	Sequence	AX452868	Sequence	C 888	16.6	0.7	38	6	AX218612	Sequence	AX218612	Sequence
C 816	16.8	0.7	48	4	SHPCFRB	Sequence	M75129	Sheep Cysti	C 889	16.6	0.7	38	6	AX220354	Sequence	AX220354	Sequence
C 817	16.8	0.7	48	4	AR021118	Sequence	AR021118	Sequence	C 890	16.6	0.7	38	6	AX220361	Sequence	AX220361	Sequence
C 818	16.8	0.7	48	6	AR036282	Sequence	AR036282	Sequence	C 891	16.6	0.7	38	6	AX220370	Sequence	AX220370	Sequence
C 819	16.8	0.7	48	6	AR044682	Sequence	AR044682	Sequence	C 892	16.6	0.7	38	6	AX223071	Sequence	AX223071	Sequence
C 820	16.8	0.7	48	6	AX002000	Sequence	AX002000	Sequence	C 893	16.6	0.7	38	6	AX223106	Sequence	AX223106	Sequence
C 821	16.8	0.7	48	6	AX338225	Sequence	AX338225	Sequence	C 894	16.6	0.7	38	6	AX425295	Sequence	AX425295	Sequence
C 822	16.8	0.7	48	9	HS0088249	Sequence	U08249	Human chrom	C 895	16.6	0.7	38	6	AX425313	Sequence	AX425313	Sequence
C 823	16.8	0.7	48	17	HSC06F06	Sequence	X88550	H. sapiens D	C 896	16.6	0.7	38	6	AX425327	Sequence	AX425327	Sequence
C 824	16.8	0.7	49	6	AX077279	Sequence	AX077279	Sequence	C 897	16.6	0.7	38	6	AX425375	Sequence	AX425375	Sequence
C 825	16.8	0.7	49	6	AR032767	Sequence	AR032767	Sequence	C 898	16.6	0.7	39	6	AX137841	Sequence	AX137841	Sequence
C 826	16.8	0.7	50	6	AR040807	Sequence	AR040807	Sequence	C 899	16.6	0.7	39	6	AX230507	Sequence	AX230507	Sequence
C 827	16.8	0.7	50	6	AR179390	Sequence	AR179390	Sequence	C 900	16.6	0.7	39	6	AX354710	Sequence	AX354710	Sequence
C 828	16.8	0.7	50	6	AR209431	Sequence	AR209431	Sequence	C 901	16.6	0.7	39	6	AX461696	Sequence	AX461696	Sequence
C 829	16.8	0.7	50	6	AX147194	Sequence	AX147194	Sequence	C 902	16.6	0.7	39	6	E17102	Sequence	E17102	Sequence
C 830	16.8	0.7	50	6	AX157664	Sequence	AX157664	Sequence	C 903	16.6	0.7	39	6	182409	Sequence	182409	Sequence
C 831	16.8	0.7	50	6	AX160081	Sequence	AX160081	Sequence	C 904	16.6	0.7	39	11	AL807574	Sequence	AL807574	Sequence
C 832	16.8	0.7	50	6	AX160454	Sequence	AX160454	Sequence	C 905	16.6	0.7	40	6	A66341	Sequence	A66341	Sequence
C 833	16.8	0.7	50	6	AX160976	Sequence	AX160976	Sequence	C 906	16.6	0.7	40	6	AR029230	Sequence	AR029230	Sequence
C 834	16.8	0.7	50	6	AX165816	Sequence	AX165816	Sequence	C 907	16.6	0.7	40	6	AR029235	Sequence	AR029235	Sequence
C 835	16.8	0.7	50	6	AX455108	Sequence	AX455108	Sequence	C 908	16.6	0.7	40	6	AR129813	Sequence	AR129813	Sequence
C 836	16.8	0.7	50	6	AX454737	Sequence	AX454737	Sequence	C 909	16.6	0.7	40	6	AR169527	Sequence	AR169527	Sequence
C 837	16.8	0.7	50	6	AX484738	Sequence	AX484738	Sequence	C 910	16.6	0.7	40	6	AX020961	Sequence	AX020961	Sequence
C 838	16.8	0.7	50	6	E64593	Sequence	E64593	Immoblilzat	C 911	16.6	0.7	40	6	AX044258	Sequence	AX044258	Sequence
C 839	16.8	0.7	50	6	E64593	Sequence	E64593	Immoblilzat	C 912	16.6	0.7	40	6	AX044271	Sequence	AX044271	Sequence
C 840	16.8	0.7	50	6	I29507	Sequence	I29507	Sequence	C 913	16.6	0.7	40	6	AX235336	Sequence	AX235336	Sequence
C 841	16.8	0.7	50	6	I91181	Sequence	I91181	Sequence	C 914	16.6	0.7	41	6	A50147	Sequence	A50147	Sequence
C 842	16.8	0.7	50	10	M05R455Z	Sequence	M27441	Mus musculu	C 915	16.6	0.7	41	6	AR023526	Sequence	AR023526	Sequence
C 843	16.8	0.7	50	12	S1MRNA3C	Sequence	M15550	Synthetic B	C 916	16.6	0.7	41	6	AR036476	Sequence	AR036476	Sequence
C 844	16.6	0.7	24	6	A27557	Sequence	A27557	Synthetic V	C 917	16.6	0.7	41	6	AR069435	Sequence	AR069435	Sequence
C 845	16.6	0.7	24	6	144649	Sequence	144649	Sequence	C 918	16.6	0.7	41	6	AR122694	Sequence	AR122694	Sequence
C 846	16.6	0.7	25	6	AX487003	Sequence	AX487003	Sequence	C 919	16.6	0.7	41	6	HPVTYPEF	Sequence	HPVTYPEF	Sequence
C 847	16.6	0.7	27	6	AR143748	Sequence	AR143748	Sequence	C 920	16.6	0.7	41	6	HPVTYPEF	Sequence	HPVTYPEF	Sequence
C 848	16.6	0.7	27	6	AR184670	Sequence	AR184670	Sequence	C 921	16.6	0.7	41	6	HPVTYPEF	Sequence	HPVTYPEF	Sequence
C 849	16.6	0.7	29	6	AX183946	Sequence	AX183946	Sequence	C 922	16.6	0.7	42	6	AR020670	Sequence	AR020670	Sequence
C 850	16.6	0.7	31	6	AX046882	Sequence	AX046882	Sequence	C 923	16.6	0.7	42	6	AR024197	Sequence	AR024197	Sequence
C 851	16.6	0.7	31	6	AX328151	Sequence	AX328151	Sequence	C 924	16.6	0.7	42	6	AR121180	Sequence	AR121180	Sequence
C 852	16.6	0.7	32	6	A63625	Sequence	A63625	Sequence	C 925	16.6	0.7	42	6	AR160308	Sequence	AR160308	Sequence
C 853	16.6	0.7	32	6	I73771	Sequence	I73771	Sequence	C 926	16.6	0.7	42	6	AR161389	Sequence	AR161389	Sequence
C 854	16.6	0.7	33	6	AR071855	Sequence	AR071855	Sequence	C 927	16.6	0.7	42	6	AX128564	Sequence	AX128564	Sequence
C 855	16.6	0.7	33	6	AR095228	Sequence	AR095228	Sequence	C 928	16.6	0.7	42	6	BD003595	Sequence	BD003595	Sequence
C 856	16.6	0.7	33	6	AR112595	Sequence	AR112595	Sequence	C 929	16.6	0.7	43	6	A04398	Sequence	A04398	Sequence
C 857	16.6	0.7	33	6	AR125195	Sequence	AR125195	Sequence	C 930	16.6	0.7	43	6	AX053467	Sequence	AX053467	Sequence
C 858	16.6	0.7	33	6	AR206976	Sequence	AR206976	Sequence	C 931	16.6	0.7	43	6	AX077070	Sequence	AX077070	Sequence
C 859	16.6	0.7	33	6	I38832	Sequence	I38832	Sequence	C 932	16.6	0.7	43	6	AX081662	Sequence	AX081662	Sequence
C 860	16.6	0.7	33	6	I74773	Sequence	I74773	Sequence	C 933	16.6	0.7	43	6	AX483440	Sequence	AX483440	Sequence
C 861	16.6	0.7	34	6	A37274	Sequence	A37274	Sequence	C 934	16.6	0.7	43	6	AX483529	Sequence	AX483529	Sequence
C 862	16.6	0.7	34	6	AR095299	Sequence	AR095299	Sequence	C 935	16.6	0.7	43	6	AX484412	Sequence	AX484412	Sequence
C 863	16.6	0.7	34	6	AR103402	Sequence	AR103402	Sequence	C 936	16.6	0.7	43	6	AX484559	Sequence	AX484559	Sequence
C 864	16.6	0.7	34	6	AR103983	Sequence	AR103983	Sequence	C 937	16.6	0.7	43	14	STVMONTAXA	Sequence	STVMONTAXA	Sequence
C 865	16.6	0.7	34	6	AR112964	Sequence	AR112964	Sequence	C 938	16.6	0.7	44	6	AR021002	Sequence	AR021002	Sequence
C 866	16.6	0.7	34	6	AR112980	Sequence	AR112980	Sequence	C 939	16.6	0.7	44	6	AR043417	Sequence	AR043417	Sequence
C 867	16.6	0.7	34	6	165590	Sequence	165590	Sequence	C 940	16.6	0.7	44	6	AR062332	Sequence	AR062332	Sequence
C 868	16.6	0.7	35	6	AR136902	Sequence	AR136902	Sequence	C 941	16.6	0.7	44	6	AR161437	Sequence	AR161437	Sequence

C 942	16.6	0.7	44	6	AR183791	Sequence
C 943	16.6	0.7	44	6	AX074211	Sequence
C 944	16.6	0.7	44	6	I29886	Sequence 23
C 945	16.6	0.7	44	6	I81453	Sequence 12
C 946	16.6	0.7	44	6	HMTCBVJ3	Sequence 12
C 947	16.6	0.7	45	6	AR100705	Sequence
C 948	16.6	0.7	45	6	AX151011	Sequence
C 949	16.6	0.7	45	6	I06248	Sequence 6
C 950	16.6	0.7	46	6	AX403764	Sequence
C 951	16.6	0.7	46	6	AX452009	Sequence
C 952	16.6	0.7	47	6	A98778	Sequence 11
C 953	16.6	0.7	47	6	AR079493	Sequence
C 954	16.6	0.7	47	6	AR086674	Sequence
C 955	16.6	0.7	47	6	AR086675	Sequence
C 956	16.6	0.7	47	6	AR211828	Sequence
C 957	16.6	0.7	47	6	AX194701	Sequence
C 958	16.6	0.7	47	6	AX378252	Sequence
C 959	16.6	0.7	47	8	SPU24SNOR	Sequence
C 960	16.6	0.7	47	8	HM1CA06	Sequence 16
C 961	16.6	0.7	48	6	A59028	Sequence 17
C 962	16.6	0.7	48	6	AR071849	Sequence
C 963	16.6	0.7	48	6	AR083362	Sequence
C 964	16.6	0.7	48	6	AR112589	Sequence
C 965	16.6	0.7	48	6	AR134560	Sequence
C 966	16.6	0.7	48	6	AX274422	Sequence
C 967	16.6	0.7	48	9	HSBT11158	Sequence
C 968	16.6	0.7	48	9	MDMDND48	Sequence
C 969	16.6	0.7	48	10	MDMDND48	Sequence
C 970	16.6	0.7	49	1	ECOINSM	Sequence
C 971	16.6	0.7	49	6	AR010283	Sequence
C 972	16.6	0.7	49	6	AR050282	Sequence
C 973	16.6	0.7	49	6	AX060057	Sequence
C 974	16.6	0.7	49	6	AX279844	Sequence
C 975	16.6	0.7	49	6	I61380	Sequence 9
C 976	16.6	0.7	50	5	CHKDCG	Sequence
C 977	16.6	0.7	50	6	AR032950	Sequence
C 978	16.6	0.7	50	6	AR209614	Sequence
C 979	16.6	0.7	50	6	AX081669	Sequence
C 980	16.6	0.7	50	6	AX157140	Sequence
C 981	16.6	0.7	50	6	AX157596	Sequence
C 982	16.6	0.7	50	6	AX159206	Sequence
C 983	16.6	0.7	50	6	AX160048	Sequence
C 984	16.6	0.7	50	6	AX160204	Sequence
C 985	16.6	0.7	50	6	AX160461	Sequence
C 986	16.6	0.7	50	6	AX160548	Sequence
C 987	16.6	0.7	50	6	AX160550	Sequence
C 988	16.6	0.7	50	6	AX160968	Sequence
C 989	16.6	0.7	50	6	AX165844	Sequence
C 990	16.6	0.7	50	6	AX165872	Sequence
C 991	16.6	0.7	50	6	I29690	Sequence 56
C 992	16.6	0.7	50	6	I42228	Sequence 41
C 993	16.6	0.7	50	6	I91364	Sequence 56
C 994	16.6	0.7	50	9	AF057511	Sequence
C 995	16.6	0.7	50	9	AF098331	Sequence
C 996	16.6	0.7	50	9	HUMSAU3466	Sequence
C 997	16.6	0.7	50	9	HSU96944	Sequence
C 998	16.6	0.7	50	9	HSU96945	Sequence
C 999	16.6	0.7	50	10	AF071645	Sequence
C 1000	16.6	0.7	50	10	MMU41938	Sequence

## ALIGNMENTS

RESULT 1  
LOCUS AR091202/c  
DEFINITION Sequence 1322 from patent US 594076.  
ACCESSION AR091202  
VERSION AR091202.1 GI:10017957  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

28 bp DNA  
linear PAT 07-SEP-2000

REFERENCE 1 (bases 1 to 28)  
AUTHORS Chenchik, A., Jorkhadze, G. and Bibilashvili, R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 594076-A 1322 30-NOV-1999;  
FEATURES  
source Location/Qualifiers  
1..28  
/organism="unknown"  
BASE COUNT 8 a 5 c 9 g 6 t  
ORIGIN

Query Match 1.2%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 CTTGAGTCTCAGTCTGATGACCCACAC 886  
Db 28 CTTGAGTCTCAGTCTGATGACCCACAC 1

RESULT 2  
LOCUS AR198237/c  
DEFINITION Sequence 1322 from patent US 6352829.  
ACCESSION AR198237  
VERSION AR198237.1 GI:20248086  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Chenchik, A., Jorkhadze, G. and Bibilashvili, R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 6352829-A 1322 05-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..28  
/organism="unknown"

BASE COUNT 8 a 5 c 9 g 6 t  
ORIGIN

Query Match 1.2%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 CTTGAGTCTCAGTCTGATGACCCACAC 886  
Db 28 CTTGAGTCTCAGTCTGATGACCCACAC 1

RESULT 3  
LOCUS AR121773  
DEFINITION Sequence 37 from patent US 6160095.  
ACCESSION AR121773  
VERSION AR121773.1 GI:14105349  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Chaudhary, P. M. and Hood, L.  
TITLE Proteins capable of regulating NF- $\kappa$ B, JNK and apoptosis  
pathways and methods of using the same  
JOURNAL Patent: US 6160095-A 37 12-DEC-2000;  
FEATURES  
source Location/Qualifiers  
1..29  
/organism="unknown"

BASE COUNT 6 a 8 c 9 g 6 t  
ORIGIN

Query Match 1.2%; Score 27.4; DB 6; Length 29;  
Best Local Similarity 96.6%; Pred. No. 7.5e+04;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 585 TCTTCATTGAGGCTGCGGAGGAGCCGAG 613  
Db 1 TCTTCATTGAGGCTGCGGAGGAGCCGAG 29

RESULT 4  
ARI121774/c  
LOCUS ARI121774 29 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 38 from patent US 6160095.  
ACCESSION ARI121774  
VERSION ARI121774.1 GI:14105350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Chaudhary,P.M. and Hood,L.  
TITLE Proteins capable of regulating NF-kappa.B, JNK and apoptosis  
pathways and methods of using the same  
JOURNAL Patent: US 6160095-A 38 12-DEC-2000;  
FEATURES  
Source Location/Qualifiers  
1..29  
/organism="unknown"

BASE COUNT 6 a 9 c 8 g 6 t  
ORIGIN

Query Match 1.2%; Score 27.4; DB 6; Length 29;  
Best Local Similarity 96.6%; Pred. No. 7.5e+04;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 585 TCTTCATTGAGGCTGCGGAGGAGCCGAG 613  
Db 29 TCTTCATTGAGGCTGCGGAGGAGCCGAG 1

RESULT 5  
AR091106/c  
LOCUS AR091106 27 bp DNA linear PAT 07-SEP-2000.  
DEFINITION Sequence 1226 from patent US 5994076.  
ACCESSION AR091106  
VERSION AR091106.1 GI:10017861  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 1226 30-NOV-1999;  
FEATURES  
Source Location/Qualifiers  
1..27  
/organism="unknown"

BASE COUNT 9 a 1 c 13 g 4 t  
ORIGIN

Query Match 1.2%; Score 27; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TCTCACCCTATCCTGCGCTCACATCTTC 1838  
Db 27 TCTCACCCTATCCTGCGCTCACATCTTC 1

RESULT 6  
ARI98141/c  
LOCUS ARI98141 27 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1226 from patent US 6352829.  
ACCESSION ARI98141  
VERSION ARI98141.1 GI:20247990  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 6352829-A 1226 05-MAR-2002;  
FEATURES  
Source Location/Qualifiers  
1..27  
/organism="unknown"

BASE COUNT 9 a 1 c 13 g 4 t  
ORIGIN

Query Match 1.2%; Score 27; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TCTCACCCTATCCTGCGCTCACATCTTC 1838  
Db 27 TCTCACCCTATCCTGCGCTCACATCTTC 1

RESULT 7  
AR091105  
LOCUS AR091105 26 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1225 from patent US 5994076.  
ACCESSION AR091105  
VERSION AR091105.1 GI:10017860  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 1225 30-NOV-1999;  
FEATURES  
Source Location/Qualifiers  
1..26  
/organism="unknown"

BASE COUNT 7 a 7 c 7 g 5 t  
ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1605 TGTTCACACACCCGCGCTATGAGCA 1630  
Db 1 TGTTCACACACCCGCGCTATGAGCA 26

RESULT 8  
AR091201  
LOCUS AR091201 26 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1321 from patent US 5994076.  
ACCESSION AR091201  
VERSION AR091201.1 GI:10017956  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 1321 30-NOV-1999;  
FEATURES  
Source Location/Qualifiers  
1..26  
/organism="unknown"

BASE COUNT 4 a 7 c 7 g 8 t  
ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGCTTGCCGAGGAC 609  
 DB 1 TTCTTCATTCAGCTTGCCGAGGAC 26

RESULT 9  
 ARI98140  
 LOCUS ARI98140 26 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 1225 from patent US 6352829.  
 ACCESSION ARI98140  
 VERSION ARI98140.1 GI:20247989  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,I.R.  
 TITLE Methods of assaying differential expression  
 JOURNAL Patent: US 6352829-A 1225 05-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..26  
 /organism="unknown"

BASE COUNT 7 a 7 c 7 g 5 t  
 ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 TGTTCACACCCAGGCTATGAGA 1630  
 DB 1 TGTTCACACCCAGGCTATGAGA 26

RESULT 10  
 ARI98236  
 LOCUS ARI98236 26 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 1321 from patent US 6352829.  
 ACCESSION ARI98236  
 VERSION ARI98236.1 GI:20248085  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,I.R.  
 TITLE Methods of assaying differential expression  
 JOURNAL Patent: US 6352829-A 1321 05-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..26  
 /organism="unknown"

BASE COUNT 4 a 7 c 7 g 8 t  
 ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGCTTGCCGAGGAC 609  
 DB 1 TTCTTCATTCAGCTTGCCGAGGAC 26

RESULT 11  
 AX207739/c  
 LOCUS AX207739 48 bp DNA linear PAT 31-AUG-2001  
 DEFINITION Sequence 37 from patent WO0157242.  
 ACCESSION AX207739  
 VERSION AX207739.1 GI:15422423  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct

artificial sequences.  
 1 (bases 1 to 48)  
 AUTHORS Stack,J.H., Whitney,M., Cubitt,A.B. and Pollok,B.A.  
 TITLE Methods of protein destabilization and uses thereof  
 JOURNAL Patent: WO 0157242-A 37 09-AUG-2001;  
 Aurora Biosciences Corporation (US)  
 FEATURES Location/Qualifiers  
 source 1..48  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Primer for PCR"

BASE COUNT 17 a 7 c 11 g 13 t  
 ORIGIN

Query Match 1.1%; Score 25.6; DB 6; Length 48;  
 Best Local Similarity 77.5%; Pred. No. 2.1e+05;  
 Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 912 GTGTGTCCTCATGCTCACCAAGAACTCTACTCAGTCA 951  
 DB 48 GTATGTTTCATGCTCTCACAAAGAACTCTATTATTATCA 9

RESULT 13  
 A59018  
 LOCUS A59018 48 bp DNA linear PAT 06-MAR-1998  
 DEFINITION Sequence 6 from Patent EP0753581.  
 ACCESSION A59018  
 VERSION A59018.1 GI:3714453  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 48)  
 AUTHORS Schefflinger,F.D., Antoline,G.D., Falkner, Falco-Guenter,D.,  
 Dornier,F.P. and Elbl,J.D.  
 TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for  
 their production and their use as vaccines  
 JOURNAL Patent: EP 0753581-A 6 15-JAN-1997;  
 IMMUNO AG (AT)  
 FEATURES Location/Qualifiers



RESULT 18  
LOCUS A59017/c 46 bp DNA linear PAT 06-MAR-1998  
DEFINITION Sequence 5 from Patent EP0753581.  
ACCESSION A59017  
VERSION A59017.1 GI:3714452  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,  
Dorner, F.P. and Eibl, J.D.  
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for  
their production and their use as vaccines  
JOURNAL Patent: EP 0753581-A 5 15-JAN-1997;  
IMMUNO AG (AT)  
FEATURES  
source Location/Qualifiers  
1..46  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 21 a 3 c 5 g 17 t  
ORIGIN

Query Match 0.9%; Score 21.8; DB 6; Length 46;  
Best Local Similarity 70.7%; Pred. No. 1.8e+06;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy. 2063 TGCAAAATCTGTTATGCTTAAATATATCTGACTTTT 2103  
Db 46 TGTTACTTATTTATGATGATGAAATATATTTTCAACTTTT 6

RESULT 19  
LOCUS S82866S2 47 bp DNA linear ROD 11-FEB-1997  
DEFINITION Apod-apolipoprotein D (5' region) [mice, 129/Svj, genomic, 47 nt,  
segment 2 of 2].  
ACCESSION S82867  
VERSION S82867.1 GI:1836133  
KEYWORDS  
SEGMENT  
SOURCE 2 of 2  
ORGANISM Mus sp. 129/Svj.  
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murine; Mus.  
1 (bases 1 to 47)  
AUTHORS Yoshida, K., Cleaveland, E.S., Nagle, J.W., French, S., Yaswen, L.,  
Oshima, T., Brady, R.O., Pentchev, P.G. and Kulkarni, A.B.  
TITLE Molecular cloning of the mouse apolipoprotein D gene and its  
upregulated expression in Niemann-Pick disease type C mouse model  
JOURNAL DNA Cell Biol. 15 (10), 873-882 (1996)  
MEDLINE 97047918  
PUBMED 8892759  
REMARK Genbank staff at the National Library of Medicine created this  
entry [NCBI gidsq 179317] from the original journal article.  
This sequence comes from Fig. 1B.  
FEATURES  
source Location/Qualifiers  
1..47  
/organism="Mus sp."  
/db\_xref="taxon:10095"  
join(s82866.1:493..536,S82866.1:620..689,11..>47)  
39..47  
/partial  
/gene="Apod"  
/note="apolipoprotein D"  
39..47  
/partial  
/gene="Apod"  
/codon\_start=1  
BASE COUNT 8 a 23 c 8 g 8 t  
ORIGIN

Query Match 0.9%; Score 21.8; DB 10; Length 47;  
Best Local Similarity 78.8%; Pred. No. 1.8e+06;  
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1850 TACTGCCGAGGCTATCTGAGAGCCACCTCACC 1882  
Db 1 TTCTCCCGAGGCTCTCTCTGAGCCACCCACC 33

RESULT 20  
LOCUS AR207719 49 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 59 from patent US 6379897.  
ACCESSION AR207719  
VERSION AR207719.1 GI:21507547  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Weidenhammer, E.M., Wang, L., Xu, X., Heller, M.J. and Kahl, B.F.  
TITLE Methods for gene expression monitoring on electronic microarrays  
JOURNAL Patent: US 6379897-A 59 30-APR-2002;  
FEATURES  
source Location/Qualifiers  
1..49  
/organism="unknown"  
BASE COUNT 20 a 5 c 12 g 12 t  
ORIGIN

Query Match 0.9%; Score 21.8; DB 6; Length 49;  
Best Local Similarity 70.7%; Pred. No. 1.8e+06;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1979 TGACAAATTTATCCATTCATTCATTTATTCATTTGGGTTGTC 2019  
Db 46 TCATTCATTCATTCATTCATTCATTCATTCATTCATTCAGTGC 6

RESULT 21  
LOCUS A59014 49 bp DNA linear PAT 06-MAR-1998  
DEFINITION Sequence 2 from Patent EP0753581.  
ACCESSION A59014  
VERSION A59014.1 GI:3714449  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,  
Dorner, F.P. and Eibl, J.D.  
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for  
their production and their use as vaccines  
JOURNAL Patent: EP 0753581-A 2 15-JAN-1997;  
IMMUNO AG (AT)  
FEATURES  
source Location/Qualifiers  
1..49  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 17 a 8 c 3 g 21 t  
ORIGIN

Query Match 0.9%; Score 21.6; DB 6; Length 49;  
Best Local Similarity 68.2%; Pred. No. 2e+06;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 2060 ATGTGCAAAATCTGTTATGCTTAAATATATCTGACTTTT 2103  
Db 2 ATTGCTTAATTTATGATGATGAAATATATTTTCAACTTTT 45

RESULT 22  
ARI24897/c

LOCUS AR124897 45 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 27 from patent US 6172213.  
 ACCESSION AR124897  
 VERSION AR124897.1 GI:14110258  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 45)  
 AUTHORS Lowman,H.B., Presta,L.G., Jardieu,P.M. and Lowe,J.  
 TITLE Anti-1Ige antibodies and method of improving polypeptides  
 JOURNAL Patent: US 6172213-A 27 09-JAN-2001;  
 FEATURES Location/Qualifiers  
 source 1..45  
 /organism="unknown"  
 BASE COUNT 15 a 9 c 10 g 11 t  
 ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 45;  
 Best Local Similarity 71.8%; Pred. No. 2.2e+06;  
 Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1201 CTGTTACCTGTTAATAGACTTAATACATGCAACAGAG 1239  
 Db 41 CTATCACCTCTTATTAAGACTTATTAAGTGCAGCGCAG 3

RESULT 23  
 LOCUS AR134560 48 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 9 from patent US 6194155.  
 ACCESSION AR134560  
 VERSION AR134560.1 GI:14123465  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 48)  
 AUTHORS Cohen,J.  
 TITLE Computerized method of identifying and locating resonating,  
 self-hybridizing nucleic acid elements  
 JOURNAL Patent: US 6194155-A 9 27-FEB-2001;  
 FEATURES Location/Qualifiers  
 source 1..48  
 /organism="unknown"  
 BASE COUNT 20 a 7 c 5 g 16 t  
 ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 48;  
 Best Local Similarity 71.8%; Pred. No. 2.2e+06;  
 Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1023 CTCCTGAATATTCGAAATTCCTCAGGATTTAATTTC 1061  
 Db 2 CTCCTGAATATTTAGAAAGAACTGACGACATCAATTC 40

RESULT 24  
 LOCUS AX094703 47 bp DNA linear PAT 30-MAR-2001  
 DEFINITION Sequence 827 from Patent WO0118547.  
 ACCESSION AX094703  
 VERSION AX094703.1 GI:13510921  
 KEYWORDS  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 47)  
 AUTHORS Davies,R.W., Kaiser,K.U. and Yang,M.Y.  
 TITLE Essential genes and assays relating thereto  
 JOURNAL Patent: WO 0118547-A 827 15-MAR-2001;

THE UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW (GB)  
 FEATURES Location/Qualifiers  
 source 1..47  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 misc-feature complement(1..47)  
 /note="Area matching Drosophila genomic sequence AC005130.  
 Matches in area of 826AA predicted protein. Sequence  
 similarity to Helix-loop-helix genes. Drosophila ESTs  
 AA949050 and AA817663 come from this gene"  
 BASE COUNT 13 a 6 c 9 g 19 t  
 ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 47;  
 Best Local Similarity 69.0%; Pred. No. 2.5e+06;  
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2041 AACCAATCTGTTGGCTTATGTGCAAAATCTGTATAGCTT 2082  
 Db 5 AGCCATATTACTGTTGTTGATTTGCCAAAGTTGTAATAGATT 46

RESULT 25  
 LOCUS AR153148 48 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 150 from patent US 6235480.  
 ACCESSION AR153148  
 VERSION AR153148.1 GI:15120680  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 48)  
 AUTHORS Shultz,J.William., Lewis,M.K., Leipe,D., Mandrekar,M., Kephart,D.,  
 Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
 Olson,R.J., Wood,K.V. and Welch,R.  
 TITLE Detection of nucleic acid hybrids  
 JOURNAL Patent: US 6235480-A 150 22-MAY-2001;  
 FEATURES Location/Qualifiers  
 source 1..48  
 /organism="unknown"  
 BASE COUNT 18 a 7 c 11 g 12 t  
 ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 48;  
 Best Local Similarity 69.0%; Pred. No. 2.5e+06;  
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1985 ATTTATCATTCATCAATCATTTATTCATTTGGTTGTCAGATAGT 2026  
 Db 45 ATTCAATTCATTCATTCATTCATTCAGTGAAGGTTCCCTAAGT 4

RESULT 26  
 LOCUS AR210944 48 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 44 from patent US 6391551.  
 ACCESSION AR210944  
 VERSION AR210944.1 GI:21513807  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 48)  
 AUTHORS Shultz,J.William., Lewis,M.K., Leipe,D., Mandrekar,M., Kephart,D.,  
 Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
 Olson,R.J., Wood,K.V. and Welch,R.  
 TITLE Detection of nucleic acid hybrids  
 JOURNAL Patent: US 6391551-A 44 21-MAY-2002;  
 FEATURES Location/Qualifiers  
 source 1..48  
 /organism="unknown"  
 BASE COUNT 18 a 7 c 11 g 12 t





Query Match 0.9%; Score 20.8; DB 6; Length 43;  
Best Local Similarity 70.0%; Pred. No. 3.1e+06;  
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2047 CTGTTTGCCCTTATGCGCAAAATCTGTTAGCTTTAA 2086  
DB 42 CTTCTTGCGATTTTGTGAAAGTCTGTATAGTATAGAA 3

RESULT 31  
A46759/c A46759 49 bp DNA linear PAT 07-MAR-1997  
LOCUS Sequence 1 from Patent EP0681027.  
DEFINITION A46759  
ACCESSION A46759.1 GI:2300854  
VERSION  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 49)  
AUTHORS Frasconi, G. and Grandi, G.  
TITLE Plasmid vector and its use for the production of heterologous proteins  
JOURNAL Patent: EP 0681027-A 1 08-NOV-1995;  
COMMENT ENRICHES SPA (IT)  
FEATURES Other publication JP 7289271 951107.  
LOCATION/Qualifiers  
1..49  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 18 a 3 c 6 g 22 t  
ORIGIN  
Query Match 0.9%; Score 20.8; DB 6; Length 49;  
Best Local Similarity 64.6%; Pred. No. 3.1e+06;  
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AATCTGTTAGCTTAAATATATCTGGAACCTTTTATGATTATTC 2115  
DB 49 AATCTATATATCATTAATAAATTTCTGCAAGCAATTAATTTTCTA 2

RESULT 32  
I89340/c I89340 49 bp DNA linear PAT 10-AUG-1998  
LOCUS Sequence 1 from patent US 5721137.  
DEFINITION I89340  
ACCESSION I89340.1 GI:3409280  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 49)  
AUTHORS Frasconi, G. and Grandi, G.  
TITLE Plasmid vector and its use for the production of heterologous proteins  
JOURNAL Patent: US 5721137-A 1 24-FEB-1998;  
FEATURES Location/Qualifiers  
1..49  
/organism="unknown"

BASE COUNT 18 a 3 c 6 g 22 t  
ORIGIN

Query Match 0.9%; Score 20.8; DB 6; Length 49;  
Best Local Similarity 64.6%; Pred. No. 3.1e+06;  
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AATCTGTTAGCTTAAATATATCTGGAACCTTTTATGATTATTC 2115  
DB 49 AATCTATATATCATTAATAAATTTCTGCAAGCAATTAATTTTCTA 2

RESULT 33  
AX165053/c AX165053 50 bp DNA linear PAT 22-JUN-2001  
LOCUS Sequence 248 from patent WO0138586.  
DEFINITION AX165053  
ACCESSION AX165053  
VERSION AX165053.1 GI:14545882  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0138586-A 248 31-MAY-2001;  
FEATURES Curagen Corporation (US)  
LOCATION/Qualifiers  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26"  
Accession number c943992566  
26  
variation /note="single nucleotide polymorphism"

BASE COUNT 26 a 5 c 7 g 12 t  
ORIGIN

Query Match 0.9%; Score 20.8; DB 6; Length 50;  
Best Local Similarity 70.0%; Pred. No. 3.1e+06;  
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2220 AATCTGATAATGACGCTTTTCTGCGCAATATAGTA 2259  
DB 43 AATCTTGTAATGCTCTTTTCTGCTCAGATTTA 4

RESULT 34  
ARI39408/c ARI39408 41 bp DNA linear PAT 16-JUN-2001  
LOCUS Sequence 21 from patent US 6207373.  
DEFINITION ARI39408  
ACCESSION ARI39408  
VERSION ARI39408.1 GI:14481904  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41)  
AUTHORS Sosnowski, R.G. and Tu, E.  
TITLE Methods for determining nature of repeat units in DNA  
JOURNAL Patent: US 6207373-A 21 27-MAR-2001;  
FEATURES Location/Qualifiers  
1..41  
/organism="unknown"

BASE COUNT 16 a 5 c 10 g 10 t  
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 41;  
Best Local Similarity 74.3%; Pred. No. 3.4e+06;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATCCATTCATTCATTTATTCATTCGCTGTC 2019  
DB 40 ATTATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 35  
ARI39392/c ARI39392 45 bp DNA linear PAT 16-JUN-2001  
LOCUS Sequence 5 from patent US 6207373.  
DEFINITION ARI39392  
ACCESSION ARI39392.1 GI:14481888  
VERSION





DEFINITION DNA encoding fructosylamino acid oxidase.  
ACCESSION E22339  
VERSION E22339.1 GI:13024007  
KEYWORDS JP 1999046769-A/32.  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Akio, K., Yasuyoshi, S., Yoshiki, T. and Hiroshi, F.  
TITLE DNA encoding fructosylamino acid oxidase  
JOURNAL Patent: JP 1999046769-A 32 23-FEB-1999;  
KYOTO DAITCHI KAGAKU CO LTD  
COMMENT OS Unidentified  
PN JP 1999046769-A/32  
PD 23-FEB-1999  
PF 05-AUG-1997 JP 1997210609  
PR  
PI AKIO KATO, YASUYOSHI SAKAI, YOSHIKI TANI, HIROSHI FUKUIE PC  
C12N15/09, C12N1/19, C12N9/06, C12O1/26//((C12N15/09, C12R1:80), PC  
(C12N1/19, C12R1:72), (C12N9/06, C12R1:72), C12N15/00, (C12N15/00, PC  
C12R1:80)  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key 1.50  
FT source Location/Qualifiers  
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/organism="unclassified"  
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BASE COUNT 14 a 5 c 12 g 19 t  
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Query Match 0.9%; Score 20.2; DB 6; Length 50;  
Best Local Similarity 68.3%; Pred. No. 4.4e+06;  
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 247 CAATGTCATCATATTAACACAGACACTTGTGAAGTGA 287  
DB 49 CATATCACCATCATTAACACAGACACTTGTATATTGA 9  
RESULT 44  
E22344 50 bp DNA linear PAT 18-JUN-2001  
LOCUS E22344  
DEFINITION DNA encoding fructosylamino acid oxidase.  
ACCESSION E22344  
VERSION E22344.1 GI:13024012  
KEYWORDS JP 1999046769-A/37.  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Akio, K., Yasuyoshi, S., Yoshiki, T. and Hiroshi, F.  
TITLE DNA encoding fructosylamino acid oxidase  
JOURNAL Patent: JP 1999046769-A 37 23-FEB-1999;  
KYOTO DAITCHI KAGAKU CO LTD  
COMMENT OS Unidentified  
PN JP 1999046769-A/37  
PD 23-FEB-1999  
PF 05-AUG-1997 JP 1997210609  
PR  
PI AKIO KATO, YASUYOSHI SAKAI, YOSHIKI TANI, HIROSHI FUKUIE PC  
C12N15/09, C12N1/19, C12N9/06, C12O1/26//((C12N15/09, C12R1:80), PC  
(C12N1/19, C12R1:72), (C12N9/06, C12R1:72), C12N15/00, (C12N15/00, PC  
C12R1:80)  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key 1.50  
FT source Location/Qualifiers  
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BASE COUNT 25 a 10 c 3 g 12 t  
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Query Match 0.9%; Score 20.2; DB 6; Length 50;  
Best Local Similarity 68.3%; Pred. No. 4.4e+06;  
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 247 CAATGTCATCATATTAACACAGACACTTGTGAAGTGA 287  
DB 10 CATATCACCATCATTAACACAGACACTTGTATATTGA 50  
RESULT 45  
AR084536/c 36 bp DNA linear PAT 01-SEP-2000  
LOCUS AR084536  
DEFINITION Sequence 25 from patent US 5981185.  
ACCESSION AR084536  
VERSION AR084536.1 GI:10011307  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Watson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 25 09-NOV-1999;  
FEATURES  
source Location/Qualifiers  
1..36  
/organism="unknown"  
BASE COUNT 0 a 18 c 0 g 18 t  
ORIGIN  
Query Match 0.9%; Score 20; DB 6; Length 36;  
Best Local Similarity 72.2%; Pred. No. 4.8e+06;  
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 1892 GGAAGAGCAAGGACAGTGGAGGAGGAAGAACAA 1927  
DB 36 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 1  
RESULT 46  
AX361209 38 bp DNA linear PAT 15-FEB-2002  
LOCUS AX361209  
DEFINITION Sequence 46 from Patent WO0208460.  
ACCESSION AX361209  
VERSION AX361209.1 GI:18693853  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Karlsson, F.  
TITLE Methods for detection of human papillomavirus mrna  
JOURNAL Patent: WO 0208460-A 46 31-JAN-2002;  
Norchip A/S (NO)  
FEATURES  
source Location/Qualifiers  
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/note="Oligonucleotide"  
BASE COUNT 11 a 5 c 11 g 7 t 4 others  
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Query Match 0.9%; Score 20; DB 6; Length 38;  
Best Local Similarity 71.9%; Pred. No. 4.8e+06;  
Matches 23; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 1440 AAGTTCATATGATGATTAGAGGAGAAAGCT 1471  
DB 6 AAGTGCATATGATGATGCTGRTGAGAAWAVAMCT 37

RESULT 47  
A07129/c 39 bp DNA linear PAT 25-AUG-1993  
DEFINITION Nucleotide sequence 6 from patent number EP0258067.  
ACCESSION A07129  
VERSION A07129.1 GI:411336  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Kingsman,S.M., Wilson,M.J., Cousens,D.J. and Hinchliffe,E.  
TITLE Yeast promoter  
JOURNAL Patent: EP 0258067-A 6 02-MAR-1988;  
Delta Biotechnology Limited  
LOCATION/Qualifiers  
FEATURES  
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/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 18 a 6 c 3 g 12 t  
ORIGIN

Query Match 0.9%; Score 20; DB 6; Length 39;  
Best Local Similarity 72.2%; Pred. No. 4.8e+06;  
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2177 AAGATTTTGGCAGCTTTTCAAGATGTCGTA 2212  
Db 37 AAGATCTTTGGACATGTTATATATTGTTGTA 2

RESULT 48  
E03833/c 46 bp DNA linear PAT 29-SEP-1997  
LOCUS E03833  
DEFINITION DNA encoding probe for gaining human thrombomodulin gene.  
ACCESSION E03833.1 GI:2172047  
VERSION JP 1992210700-A/1.  
KEYWORDS JP 1992210700-A/1.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Sakano,K., Fujiwara,H., Sugiyama,N., Nawa,K. and Marumoto,Y.  
TITLE RECOMBINANT HUMAN THROMBOMODULIN DERIVATIVE  
JOURNAL Patent: JP 1992210700-A 1 31-JUL-1992;  
DAI ICHI SEIYAKU CO LTD  
OS Artificial gene  
OC Artificial sequence; Genes.  
PN JP 1992210700-A/1  
PD 31-JUL-1992  
PF 12-DEC-1990 JP 1990409855  
PI SAKANO KATSUICHI, FUJIWARA HIROYUKI, SUGIYAMA NORIBUMI, PI  
NAWA KATSUHIKO,  
PI MARUMOTO YASUMASA  
PC C07K13/00,A61K37/02,C12N5/10,C12N15/12,C12N15/85,C12P21/02, PC  
(C12N5/10,  
PC C12R1.91),(C12N15/85,C12R1.91),(C12P21/02,C12R1.91); CC  
strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
CC \*source: clone=Pr-TM-01;  
FH Key Location/Qualifiers  
FT misc\_feature 1. .46  
FT /note="DNA probe for gaining human FT  
thrombomodulin gene".  
LOCATION/Qualifiers  
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FEATURES  
source

BASE COUNT 6 a 21 c 12 g 7 t  
ORIGIN

Query Match 0.9%; Score 20; DB 6; Length 46;  
Best Local Similarity 65.9%; Pred. No. 4.9e+06;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 737 TGGAGAGCCCGAGAGAGCTCTGTTGTGCAAGCCCTCTG 780  
Db 44 TGGGGGTGAGAGGACAGGCTCTGAGAGGAGCCAGGCTCTG 1

RESULT 49  
AR059781/c 50 bp DNA linear PAT 29-SEP-1999  
LOCUS AR059781  
DEFINITION Sequence 31 from patent US 5840520.  
ACCESSION AR059781  
VERSION AR059781.1 GI:5986231  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Clarke,D.,Kirkwood, and Palese,P.M.  
TITLE Recombinant negative strand RNA virus expression systems  
JOURNAL Patent: US 5840520-A 31 24-NOV-1998;  
LOCATION/Qualifiers  
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/organism="unknown"  
BASE COUNT 24 a 6 c 7 g 13 t  
ORIGIN

Query Match 0.9%; Score 20; DB 6; Length 50;  
Best Local Similarity 65.9%; Pred. No. 4.9e+06;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2083 TAAATATATCTGGAACCTTTTACATTAATCCAGCCCTATTTT 2126  
Db 48 TTAATTAAAGTGGTACTTATCAATTTCTTATTTGCCCATTTT 5

RESULT 50  
E60006 45 bp DNA linear PAT 31-JAN-2002  
LOCUS E60006  
DEFINITION Ceramide-binding peptide.  
ACCESSION E60006  
VERSION E60006.1 GI:18622765  
KEYWORDS JP 2000319296-A/6.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Ishikawa,M., Tanaka,Y., Ogino,K. and Taki,T.  
TITLE Ceramide-binding peptide  
JOURNAL Patent: JP 2000319296-A 6 21-NOV-2000;  
OTSUKA PHARMACEUT CO LTD  
OS Artificial Sequence  
PN JP 2000319296-A/6  
PD 21-NOV-2000  
PF 10-MAY-1999 JP 1999128674  
PI MASARU ISHIKAWA,YOSHINORI TANAKA,KOICHI OGINO,TAKAO TAKI PC  
CC C07K7/00  
FH MASARU ISHIKAWA,YOSHINORI TANAKA,KOICHI OGINO,TAKAO TAKI PC  
FT MASARU ISHIKAWA,YOSHINORI TANAKA,KOICHI OGINO,TAKAO TAKI PC  
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LOCATION/Qualifiers  
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FEATURES  
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BASE COUNT 5 a 7 c 14 g 19 t  
ORIGIN



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OM nucleic - nucleic search, using sw model

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Title: US-09-659-860A-3

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Searched: 441362 seqs, 15338381 residues

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Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	28	1.2	28	4	US-09-225-928-1322
C 3	27.4	1.2	29	4	US-09-382-155-37
C 4	27.4	1.2	29	4	US-09-382-155-38
C 5	27	1.2	27	2	US-08-859-998-1226
C 6	27	1.2	27	2	US-09-225-928-1226
C 7	26	1.1	26	2	US-08-859-998-1225
C 8	26	1.1	26	2	US-08-859-998-1321
C 9	26	1.1	26	4	US-09-225-928-1225
C 10	26	1.1	26	4	US-09-225-928-1321
C 11	22.8	1.0	41	4	US-09-171-162B-11
C 12	22.8	1.0	49	4	US-09-030-156-6
C 13	22.8	1.0	49	4	US-09-645-757-6
C 14	21.8	0.9	37	4	US-09-171-162B-12
C 15	21.8	0.9	38	4	US-09-545-481-7
C 16	21.8	0.9	49	4	US-09-710-200-59
C 17	21.4	0.9	45	4	US-09-109-207C-27
C 18	21.4	0.9	48	4	US-09-305-408-9
C 19	21.2	0.9	48	4	US-09-358-972-150
C 20	21.2	0.9	48	4	US-09-383-316-44
C 21	21	0.9	21	4	US-08-556-627A-7
C 22	20.8	0.9	41	4	US-09-564-805-130
C 23	20.8	0.9	49	1	US-08-400-864-1
C 24	20.6	0.9	41	4	US-09-030-156-21
C 25	20.6	0.9	41	4	US-09-645-757-21
C 26	20.6	0.9	45	4	US-09-030-156-5
C 27	20.6	0.9	45	4	US-09-645-757-5

28	20.2	0.9	47	4	US-09-641-638-1284	Sequence 1284, Ap
C 29	20.2	0.9	50	1	US-07-828-444-7	Sequence 7, Appl
C 30	20	0.9	36	2	US-08-863-639A-25	Sequence 25, Appl
C 31	20	0.9	42	3	US-08-938-830-31	Sequence 31, Appl
C 32	20	0.9	47	4	US-09-641-638-1118	Sequence 1118, Ap
C 33	20	0.9	50	2	US-08-316-439A-31	Sequence 31, Appl
C 34	19.8	0.9	43	4	US-09-276-533A-6	Sequence 6, Appl
C 35	19.8	0.9	47	4	US-09-158-863C-32	Sequence 32, Appl
C 36	19.6	0.8	31	4	US-09-171-162B-13	Sequence 13, Appl
C 37	19.6	0.8	42	5	PCT-US96-03916-35	Sequence 35, Appl
C 38	19.6	0.8	49	2	US-08-801-898A-27	Sequence 27, Appl
C 39	19.4	0.8	21	4	US-08-556-627A-9	Sequence 9, Appl
C 40	19.4	0.8	40	1	US-08-231-342-17	Sequence 17, Appl
C 41	19.4	0.8	47	4	US-09-345-882-71	Sequence 71, Appl
C 42	19.2	0.8	36	3	US-08-843-409-11	Sequence 11, Appl
C 43	19.2	0.8	41	2	US-08-484-397A-17	Sequence 17, Appl
C 44	19.2	0.8	41	4	US-09-546-483-2	Sequence 2, Appl
C 45	19.2	0.8	41	4	US-09-823-177-2	Sequence 2, Appl
C 46	19.2	0.8	42	3	US-08-746-111-40	Sequence 40, Appl
C 47	19.2	0.8	45	4	US-09-284-832-29	Sequence 29, Appl
C 48	19.2	0.8	47	4	US-09-641-638-931	Sequence 931, Appl
C 49	19.2	0.8	48	1	US-08-471-791-35	Sequence 35, Appl
C 50	19.2	0.8	48	5	PCT-US91-01746-35	Sequence 35, Appl
C 51	19.2	0.8	50	4	US-09-315-886C-13	Sequence 13, Appl
C 52	19.2	0.8	50	4	US-08-973-005A-2	Sequence 2, Appl
C 53	19	0.8	19	4	US-08-556-627A-5	Sequence 5, Appl
C 54	19	0.8	41	3	US-08-813-507-35	Sequence 35, Appl
C 55	19	0.8	45	3	US-09-464-453-35	Sequence 35, Appl
C 56	19	0.8	45	4	US-08-213-741-6	Sequence 6, Appl
C 57	19	0.8	45	4	US-08-522-336-6	Sequence 6, Appl
C 58	19	0.8	46	4	US-09-537-357-8	Sequence 48, Appl
C 59	19	0.8	48	3	US-08-933-358-10	Sequence 20, Appl
C 60	19	0.8	49	2	US-08-980-071-74	Sequence 74, Appl
C 61	19	0.8	49	2	US-08-980-071-75	Sequence 75, Appl
C 62	19	0.8	49	3	US-09-314-093-74	Sequence 74, Appl
C 63	19	0.8	49	3	US-09-314-093-75	Sequence 75, Appl
C 64	19	0.8	49	4	US-09-337-635-74	Sequence 74, Appl
C 65	19	0.8	49	4	US-09-337-635-75	Sequence 75, Appl
C 66	19	0.8	49	4	US-09-337-280-74	Sequence 74, Appl
C 67	19	0.8	49	4	US-09-337-280-75	Sequence 75, Appl
C 68	19	0.8	50	1	US-08-513-764-3	Sequence 3, Appl
C 69	18.8	0.8	38	2	US-08-292-620A-2366	Sequence 2366, Ap
C 70	18.8	0.8	38	3	US-09-071-845-2366	Sequence 2366, Ap
C 71	18.8	0.8	46	1	US-08-222-177A-449	Sequence 349, Appl
C 72	18.8	0.8	48	1	US-08-171-389-226	Sequence 226, Appl
C 73	18.8	0.8	48	1	US-08-123-936-226	Sequence 226, Appl
C 74	18.8	0.8	48	2	US-08-475-228A-226	Sequence 226, Appl
C 75	18.8	0.8	48	3	US-08-482-080A-226	Sequence 226, Appl
C 76	18.8	0.8	48	4	US-09-354-947-226	Sequence 226, Appl
C 77	18.8	0.8	48	5	PCT-US93-12388-226	Sequence 226, Appl
C 78	18.8	0.8	50	2	US-08-190-199A-4	Sequence 4, Appl
C 79	18.8	0.8	50	2	US-08-316-439A-37	Sequence 37, Appl
C 80	18.6	0.8	34	3	US-08-793-666-3	Sequence 3, Appl
C 81	18.6	0.8	39	4	US-09-535-754-13	Sequence 13, Appl
C 82	18.6	0.8	40	1	US-07-854-596B-13	Sequence 13, Appl
C 83	18.6	0.8	40	2	US-09-076-193-1	Sequence 1, Appl
C 84	18.6	0.8	40	4	US-09-307-925-1	Sequence 1, Appl
C 85	18.6	0.8	41	4	US-09-030-156-4	Sequence 4, Appl
C 86	18.6	0.8	41	4	US-09-645-757-4	Sequence 4, Appl
C 87	18.6	0.8	42	1	US-08-253-877C-50	Sequence 50, Appl
C 88	18.6	0.8	42	2	US-08-452-164A-50	Sequence 50, Appl
C 89	18.6	0.8	50	1	US-08-171-389-467	Sequence 467, Appl
C 90	18.6	0.8	50	1	US-08-171-389-469	Sequence 467, Appl
C 91	18.6	0.8	50	1	US-08-123-936-467	Sequence 467, Appl
C 92	18.6	0.8	50	1	US-08-123-936-469	Sequence 469, Appl
C 93	18.6	0.8	50	2	US-08-475-228A-467	Sequence 467, Appl
C 94	18.6	0.8	50	2	US-08-475-228A-469	Sequence 469, Appl
C 95	18.6	0.8	50	2	US-08-053-451B-95	Sequence 95, Appl
C 96	18.6	0.8	50	3	US-08-482-080A-467	Sequence 467, Appl
C 97	18.6	0.8	50	3	US-08-482-080A-469	Sequence 469, Appl
C 98	18.6	0.8	50	4	US-09-354-947-467	Sequence 467, Appl
C 99	18.6	0.8	50	4	US-09-354-947-469	Sequence 469, Appl
C 100	18.6	0.8	50	5	PCT-US93-12388-467	Sequence 467, Appl

C 101	18.6	0.8	50	5	PCT-US93-12388-469	Sequence 469, App	C 174	17.8	0.8	45	1	US-08-123-936-192	Sequence 192, App
C 102	18.4	0.8	40	1	US-09-083-409B-14	Sequence 14, Appl	C 175	17.8	0.8	45	2	US-08-305-766C-20	Sequence 20, Appl
C 103	18.4	0.8	50	1	US-08-316-293-45	Sequence 45, Appl	C 176	17.8	0.8	45	3	US-08-475-228A-192	Sequence 192, App
C 104	18.4	0.8	50	4	US-09-554-511-4	Sequence 4, Appl1	C 177	17.8	0.8	45	2	US-08-482-080A-192	Sequence 192, App
C 105	18.2	0.8	32	4	US-09-091-725-4	Sequence 4, Appl1	C 178	17.8	0.8	45	4	US-08-894-727-7	Sequence 7, Appl1
C 106	18.2	0.8	33	1	US-08-869-506-8	Sequence 8, Appl1	C 179	17.8	0.8	45	4	US-08-979-608A-30	Sequence 30, Appl
C 107	18.2	0.8	33	3	US-09-128-967-8	Sequence 8, Appl1	C 180	17.8	0.8	45	4	US-09-354-947-192	Sequence 192, App
C 108	18.2	0.8	36	1	US-07-807-529A-58	Sequence 58, Appl	C 181	17.8	0.8	45	5	PCT-US93-12388-192	Sequence 192, App
C 109	18.2	0.8	36	3	US-08-300-928C-97	Sequence 97, Appl	C 182	17.8	0.8	46	1	US-08-462-388-8	Sequence 8, Appl
C 110	18.2	0.8	36	3	US-08-430-944D-97	Sequence 97, Appl	C 183	17.8	0.8	47	3	US-08-448-446B-12	Sequence 12, Appl
C 111	18.2	0.8	36	3	US-08-430-014-97	Sequence 97, Appl	C 184	17.8	0.8	47	4	US-09-345-882-50	Sequence 50, Appl
C 112	18.2	0.8	36	3	US-08-431-184-97	Sequence 97, Appl	C 185	17.8	0.8	48	1	US-08-171-389-195	Sequence 195, App
C 113	18.2	0.8	39	1	US-08-634-060-59	Sequence 59, Appl	C 186	17.8	0.8	48	1	US-08-123-936-195	Sequence 195, App
C 114	18.2	0.8	41	1	US-08-191-866D-91	Sequence 91, Appl	C 187	17.8	0.8	48	2	US-08-475-228A-195	Sequence 195, App
C 115	18.2	0.8	41	3	US-08-480-640A-143	Sequence 143, App	C 188	17.8	0.8	48	3	US-08-482-080A-195	Sequence 195, App
C 116	18.2	0.8	41	3	US-08-295-802-143	Sequence 143, App	C 189	17.8	0.8	48	4	US-09-069-821-32	Sequence 32, Appl
C 117	18.2	0.8	41	4	US-08-686-968C-70	Sequence 70, App	C 190	17.8	0.8	48	4	US-09-354-947-195	Sequence 195, App
C 118	18.2	0.8	41	4	US-08-488-237A-143	Sequence 143, App	C 191	17.8	0.8	48	5	US-09-545-244A-8	Sequence 8, Appl1
C 119	18.2	0.8	41	4	US-08-375-992A-143	Sequence 143, App	C 192	17.8	0.8	48	5	PCT-US93-12388-195	Sequence 195, App
C 120	18.2	0.8	43	4	US-09-586-719-18	Sequence 18, Appl	C 193	17.8	0.8	49	1	US-07-977-438-32	Sequence 32, Appl
C 121	18.2	0.8	48	4	US-09-091-814-115	Sequence 11, Appl	C 194	17.8	0.8	49	1	US-08-458-813-32	Sequence 32, Appl
C 122	18.2	0.8	48	4	US-08-589-109A-11	Sequence 11, Appl	C 195	17.8	0.8	49	5	US-08-706-945D-56	Sequence 56, Appl
C 123	18.2	0.8	49	5	PCT-US94-0905B-5	Sequence 5, Appl1	C 196	17.8	0.8	49	5	PCT-US91-07035-32	Sequence 32, Appl
C 124	18.2	0.8	50	3	US-08-985-162-1700	Sequence 11, Appl	C 197	17.6	0.8	24	4	US-09-025-639-6	Sequence 6, Appl1
C 125	18	0.8	50	3	US-08-556-627A-8	Sequence 8, Appl	C 198	17.6	0.8	28	1	US-08-579-667-17	Sequence 17, Appl
C 126	18	0.8	18	4	US-08-556-627A-11	Sequence 11, Appl	C 199	17.6	0.8	28	3	US-08-722-719-49	Sequence 49, Appl
C 127	18	0.8	21	4	US-08-556-627A-10	Sequence 10, Appl	C 200	17.6	0.8	28	4	US-09-334-951-49	Sequence 49, Appl
C 128	18	0.8	35	1	US-08-413-118-115	Sequence 11, Appl	C 201	17.6	0.8	29	4	US-09-171-162B-14	Sequence 14, Appl
C 129	18	0.8	35	2	US-08-975-902-30	Sequence 30, Appl	C 202	17.6	0.8	35	1	US-07-854-596B-56	Sequence 56, Appl
C 130	18	0.8	35	3	US-08-473-446-115	Sequence 115, App	C 203	17.6	0.8	36	1	US-08-274-661B-33	Sequence 33, Appl
C 131	18	0.8	35	3	US-09-251-565-30	Sequence 30, Appl	C 204	17.6	0.8	36	4	US-08-420-592A-13	Sequence 13, Appl
C 132	18	0.8	36	1	US-08-399-696-41	Sequence 41, Appl	C 205	17.6	0.8	36	5	PCT-US93-03967-33	Sequence 33, Appl
C 133	18	0.8	36	1	US-08-591-989-66	Sequence 66, Appl	C 206	17.6	0.8	38	1	US-08-385-191A-7	Sequence 7, Appl1
C 134	18	0.8	36	3	US-08-781-891-185	Sequence 185, App	C 207	17.6	0.8	38	4	US-08-472-402A-7	Sequence 7, Appl1
C 135	18	0.8	38	2	US-08-467-832-4	Sequence 4, Appl1	C 208	17.6	0.8	39	1	US-08-334-773A-7	Sequence 7, Appl1
C 136	18	0.8	38	4	US-08-432-697-4	Sequence 4, Appl1	C 209	17.6	0.8	39	4	US-09-171-162B-2	Sequence 2, Appl1
C 137	18	0.8	38	4	US-08-466-248-4	Sequence 4, Appl1	C 210	17.6	0.8	40	4	US-09-141-027-18	Sequence 18, Appl
C 138	18	0.8	41	1	US-09-313-221A-20	Sequence 20, Appl	C 211	17.6	0.8	40	4	US-09-141-027-18	Sequence 18, Appl
C 139	18	0.8	42	1	US-07-967-693-36	Sequence 36, Appl	C 212	17.6	0.8	41	1	US-08-332-420-57	Sequence 57, Appl
C 140	18	0.8	42	1	US-08-195-072-34	Sequence 34, Appl	C 213	17.6	0.8	42	1	US-08-737-658B-3	Sequence 3, Appl1
C 141	18	0.8	42	1	US-08-195-735-34	Sequence 34, Appl	C 214	17.6	0.8	42	4	US-07-931-473B-4	Sequence 4, Appl1
C 142	18	0.8	42	1	US-08-195-747-34	Sequence 34, Appl	C 215	17.6	0.8	45	1	US-07-931-473B-4	Sequence 4, Appl1
C 143	18	0.8	42	1	US-08-446-884-34	Sequence 34, Appl	C 216	17.6	0.8	45	1	US-07-714-131C-4	Sequence 4, Appl1
C 144	18	0.8	42	1	US-08-195-073-34	Sequence 34, Appl	C 217	17.6	0.8	45	1	US-07-714-131C-4	Sequence 4, Appl1
C 145	18	0.8	42	1	US-08-196-175-34	Sequence 34, Appl	C 218	17.6	0.8	45	1	US-08-434-730-10	Sequence 10, Appl
C 146	18	0.8	42	2	US-08-443-153-34	Sequence 34, Appl	C 219	17.6	0.8	45	1	US-08-412-110-4	Sequence 4, Appl1
C 147	18	0.8	43	1	US-08-442-807-34	Sequence 34, Appl	C 220	17.6	0.8	45	1	US-08-409-442A-4	Sequence 4, Appl1
C 148	18	0.8	43	1	US-08-560-313A-8	Sequence 8, Appl1	C 221	17.6	0.8	45	1	US-08-409-442A-4	Sequence 4, Appl1
C 149	18	0.8	43	1	US-08-611-155B-12	Sequence 12, Appl	C 222	17.6	0.8	45	1	US-08-412-110-4	Sequence 4, Appl1
C 150	18	0.8	43	2	US-08-916-120A-14	Sequence 14, Appl	C 223	17.6	0.8	45	1	US-08-409-442A-4	Sequence 4, Appl1
C 151	18	0.8	45	1	US-08-233-009-37	Sequence 37, Appl	C 224	17.6	0.8	45	1	US-08-409-442A-4	Sequence 4, Appl1
C 152	18	0.8	45	1	US-08-233-009-38	Sequence 38, Appl	C 225	17.6	0.8	45	2	US-08-221-816B-18	Sequence 18, Appl
C 153	18	0.8	47	1	US-08-222-638B-10	Sequence 10, Appl	C 226	17.6	0.8	45	2	US-08-469-609A-4	Sequence 4, Appl
C 154	18	0.8	47	1	US-09-641-638-852	Sequence 852, App	C 227	17.6	0.8	45	2	US-08-469-609A-4	Sequence 4, Appl
C 155	18	0.8	50	3	US-08-985-162-1748	Sequence 1748, App	C 228	17.6	0.8	45	2	US-08-687-355A-13	Sequence 13, Appl
C 156	17.8	0.8	30	2	US-08-629-001A-117	Sequence 117, App	C 229	17.6	0.8	45	3	US-09-143-190-4	Sequence 4, Appl1
C 157	17.8	0.8	30	2	US-08-629-001A-117	Sequence 117, App	C 230	17.6	0.8	45	3	US-09-143-190-4	Sequence 4, Appl1
C 158	17.8	0.8	30	2	US-08-629-001A-117	Sequence 117, App	C 231	17.6	0.8	45	4	US-09-315-886C-17	Sequence 17, Appl
C 159	17.8	0.8	31	4	US-09-232-479-33	Sequence 33, Appl	C 232	17.6	0.8	45	4	US-09-502-344-4	Sequence 4, Appl
C 160	17.8	0.8	31	4	US-09-232-479-33	Sequence 33, Appl	C 233	17.6	0.8	45	4	US-09-502-344-4	Sequence 4, Appl
C 161	17.8	0.8	36	2	US-08-669-721-1	Sequence 1, Appl1	C 234	17.6	0.8	45	4	US-09-407-367-13	Sequence 13, Appl
C 162	17.8	0.8	36	2	US-08-669-721-1	Sequence 1, Appl1	C 235	17.6	0.8	47	4	US-09-641-638-805	Sequence 805, App
C 163	17.8	0.8	37	4	US-09-070-291-8	Sequence 8, Appl1	C 236	17.6	0.8	47	4	US-09-641-638-842	Sequence 842, App
C 164	17.8	0.8	38	1	US-08-373-124A-813	Sequence 813, App	C 237	17.6	0.8	48	4	US-09-641-638-858	Sequence 858, App
C 165	17.8	0.8	38	1	US-08-373-124A-813	Sequence 813, App	C 238	17.6	0.8	48	4	US-09-345-882-33	Sequence 33, Appl
C 166	17.8	0.8	38	1	US-08-435-628-813	Sequence 813, App	C 239	17.6	0.8	48	6	5240845-53	Sequence 33, Appl
C 167	17.8	0.8	38	1	US-08-435-628-813	Sequence 813, App	C 240	17.6	0.8	49	1	US-08-155-171B-27	Sequence 27, Appl
C 168	17.8	0.8	38	6	5457089-5	Patent No. 5457089	C 241	17.6	0.8	49	2	US-08-435-998-27	Sequence 27, Appl
C 169	17.8	0.8	38	6	5457089-5	Patent No. 5457089	C 242	17.6	0.8	50	1	US-08-171-389-471	Sequence 471, App
C 170	17.8	0.8	39	3	US-08-399-696-62	Sequence 62, Appl	C 243	17.6	0.8	50	1	US-08-123-936-471	Sequence 471, App
C 171	17.8	0.8	39	3	US-08-717-294-47	Sequence 47, Appl	C 244	17.6	0.8	50	2	US-08-475-228A-471	Sequence 471, App
C 172	17.8	0.8	44	4	US-08-974-549A-505	Sequence 505, App	C 245	17.6	0.8	50	2	US-08-299-074A-23	Sequence 23, Appl
C 173	17.8	0.8	45	1	US-09-011-648-2	Sequence 2, Appl1	C 246	17.6	0.8	50	3	US-08-482-080A-471	Sequence 471, App
					US-08-171-389-192	Sequence 192, App							



C 247	17.6	0.8	50	3	US-08-998-099-305	Sequence 305, App	320	17.2	0.7	49	1	US-08-466-670-5	Sequence 5, App1
C 248	17.6	0.8	50	4	US-09-399-773-23	Sequence 23, App1	321	17.2	0.7	49	2	US-08-756-506-18	Sequence 18, App1
C 249	17.6	0.8	50	4	US-09-354-947-471	Sequence 471, App	322	17.2	0.7	49	2	PCT-US95-05602-21	Sequence 21, App1
C 250	17.6	0.8	50	5	PCT-US93-12388-471	Sequence 471, App	323	17.2	0.7	49	5	PCT-US95-05816-21	Sequence 21, App1
C 251	17.4	0.8	30	2	US-08-331-081B-14	Sequence 14, App1	324	17.2	0.7	50	1	US-07-718-480-1	Sequence 1, App1
C 252	17.4	0.8	30	3	US-08-738-381-23	Sequence 23, App1	325	17.2	0.7	50	1	US-08-171-389-344	Sequence 344, App
C 253	17.4	0.8	36	1	US-07-841-662-16	Sequence 16, App1	326	17.2	0.7	50	1	US-08-171-389-390	Sequence 390, App
C 254	17.4	0.8	36	1	US-08-209-797-16	Sequence 16, App1	327	17.2	0.7	50	1	US-08-207-901-55	Sequence 55, App1
C 255	17.4	0.8	36	1	US-08-669-685-16	Sequence 16, App1	328	17.2	0.7	50	1	US-08-207-901-56	Sequence 56, App1
C 256	17.4	0.8	36	3	US-09-103-486-16	Sequence 16, App1	329	17.2	0.7	50	1	US-08-123-936-344	Sequence 344, App
C 257	17.4	0.8	36	3	US-09-039-982A-16	Sequence 16, App1	330	17.2	0.7	50	1	US-08-475-228A-390	Sequence 390, App
C 258	17.4	0.8	36	4	US-09-039-641-16	Sequence 16, App1	331	17.2	0.7	50	2	US-08-475-228A-344	Sequence 344, App
C 259	17.4	0.8	36	4	US-09-039-762A-16	Sequence 16, App1	332	17.2	0.7	50	2	US-08-475-228A-390	Sequence 390, App
C 260	17.4	0.8	36	4	US-09-042-492B-16	Sequence 16, App1	333	17.2	0.7	50	3	US-08-482-080A-344	Sequence 344, App
C 261	17.4	0.8	36	4	US-08-913-612A-16	Sequence 16, App1	334	17.2	0.7	50	3	US-08-482-080A-390	Sequence 390, App
C 262	17.4	0.8	36	5	PCT-US93-01557-16	Sequence 16, App1	335	17.2	0.7	50	4	US-09-354-947-344	Sequence 344, App
C 263	17.4	0.8	40	4	US-09-086-726-10	Sequence 10, App1	336	17.2	0.7	50	4	US-09-354-947-390	Sequence 390, App
C 264	17.4	0.8	41	4	US-09-191-468-12	Sequence 12, App1	337	17.2	0.7	50	5	PCT-US93-12388-344	Sequence 344, App
C 265	17.4	0.8	42	2	US-08-452-724A-43	Sequence 43, App1	338	17.2	0.7	50	5	PCT-US93-12388-390	Sequence 390, App
C 266	17.4	0.8	43	4	US-09-387-300-36	Sequence 36, App1	339	17.2	0.7	27	3	US-09-192-048-8	Sequence 8, App1
C 267	17.4	0.8	44	1	US-08-086-634-8	Sequence 8, App1	340	17.2	0.7	30	2	US-08-874-460-7	Sequence 7, App1
C 268	17.4	0.8	44	2	US-08-350-260A-558	Sequence 558, App	341	17.2	0.7	30	3	US-09-130-663-9	Sequence 9, App1
C 269	17.4	0.8	44	4	US-09-358-036-24	Sequence 24, App1	342	17.2	0.7	30	3	US-09-432-335-9	Sequence 9, App1
C 270	17.4	0.8	44	4	US-09-097-239-24	Sequence 24, App1	343	17.2	0.7	30	4	US-09-614-022-9	Sequence 9, App1
C 271	17.4	0.8	44	4	US-09-301-593-73	Sequence 73, App1	344	17.2	0.7	32	1	US-08-616-855-17	Sequence 17, App1
C 272	17.4	0.8	47	2	US-08-467-603-98	Sequence 98, App1	345	17.2	0.7	32	2	US-08-616-854-17	Sequence 17, App1
C 273	17.4	0.8	47	2	US-08-811-897A-51	Sequence 51, App1	346	17.2	0.7	33	2	US-08-850-049-89	Sequence 89, App1
C 274	17.4	0.8	47	2	US-08-466-793-98	Sequence 98, App1	347	17.2	0.7	33	2	US-08-050-478-89	Sequence 89, App1
C 275	17.4	0.8	47	2	US-08-855-213-51	Sequence 51, App1	348	17.2	0.7	33	4	US-09-414-117-89	Sequence 89, App1
C 276	17.4	0.8	47	2	US-08-491-861A-98	Sequence 98, App1	349	17.2	0.7	33	4	US-09-678-437-89	Sequence 89, App1
C 277	17.4	0.8	47	4	US-09-201-474-51	Sequence 51, App1	350	17.2	0.7	34	1	US-08-428-733A-22	Sequence 22, App1
C 278	17.4	0.8	47	4	US-09-641-638-1081	Sequence 1081, App	351	17.2	0.7	34	1	US-08-428-733A-25	Sequence 25, App1
C 279	17.4	0.8	50	3	US-08-985-162-1671	Sequence 1671, App	352	17.2	0.7	34	3	US-08-544-381B-174	Sequence 174, App
C 280	17.4	0.8	50	4	US-08-991-789A-269	Sequence 269, App1	353	17.2	0.7	34	3	US-08-732-708C-45	Sequence 45, App1
C 281	17.4	0.8	50	4	US-09-062-451-269	Sequence 269, App1	354	17.2	0.7	35	4	US-09-101-629A-34	Sequence 34, App1
C 282	17.4	0.8	50	4	US-08-670-186-9	Sequence 9, App1	355	17.2	0.7	35	1	US-08-364-339-10	Sequence 10, App1
C 283	17.2	0.7	31	3	US-08-848-373-1	Sequence 1, App1	356	17.2	0.7	35	1	US-08-487-034-16	Sequence 16, App1
C 284	17.2	0.7	31	3	US-08-670-186-9	Sequence 9, App1	357	17.2	0.7	35	3	US-08-577-121-23	Sequence 23, App1
C 285	17.2	0.7	31	3	US-08-848-373-1	Sequence 1, App1	358	17.2	0.7	35	3	US-08-985-700-23	Sequence 23, App1
C 286	17.2	0.7	31	5	PCT-US92-10792-29	Sequence 29, App1	359	17.2	0.7	35	5	PCT-US95-16916-23	Sequence 23, App1
C 287	17.2	0.7	33	3	US-09-023-082A-144	Sequence 144, App	360	17.2	0.7	36	2	US-08-596-387B-114	Sequence 114, App
C 288	17.2	0.7	34	4	US-09-043-646-6	Sequence 6, App1	361	17.2	0.7	36	2	US-08-374-483-9	Sequence 9, App1
C 289	17.2	0.7	35	4	US-09-266-464-4	Sequence 4, App1	362	17.2	0.7	36	4	US-09-067-615-114	Sequence 114, App
C 290	17.2	0.7	36	2	US-08-174-672D-34	Sequence 34, App1	363	17.2	0.7	36	4	US-09-420-592A-12	Sequence 12, App1
C 291	17.2	0.7	37	4	US-08-361-337-43	Sequence 43, App1	364	17.2	0.7	36	5	PCT-US95-09816A-114	Sequence 114, App
C 292	17.2	0.7	37	4	US-09-472-146A-1	Sequence 1, App1	365	17.2	0.7	38	1	US-08-105-483-402	Sequence 402, App
C 293	17.2	0.7	38	4	US-08-686-968C-98	Sequence 98, App1	366	17.2	0.7	38	1	US-08-709-209-402	Sequence 402, App
C 294	17.2	0.7	39	1	US-08-706-037-9	Sequence 9, App1	367	17.2	0.7	38	1	US-08-303-275-106	Sequence 106, App
C 295	17.2	0.7	39	1	US-08-636-876-14	Sequence 14, App1	368	17.2	0.7	38	1	US-08-458-101-402	Sequence 402, App
C 296	17.2	0.7	39	2	US-09-005-397-9	Sequence 9, App1	369	17.2	0.7	39	3	US-08-946-475-12	Sequence 12, App1
C 297	17.2	0.7	39	6	5520913-17	Patent No. 5520913	370	17.2	0.7	39	4	US-09-052-995-3	Sequence 3, App1
C 298	17.2	0.7	40	1	US-08-436-463-12	Sequence 12, App1	371	17.2	0.7	39	4	US-08-340-479-12	Sequence 12, App1
C 299	17.2	0.7	40	2	US-08-665-040-9	Sequence 9, App1	372	17.2	0.7	40	4	US-08-481-659C-22	Sequence 22, App1
C 300	17.2	0.7	40	4	US-08-189-462-25	Sequence 25, App1	373	17.2	0.7	41	4	US-09-233-086-25	Sequence 25, App1
C 301	17.2	0.7	40	4	US-09-189-462-26	Sequence 26, App1	374	17.2	0.7	41	4	US-07-723-002C-18	Sequence 18, App1
C 302	17.2	0.7	41	1	US-08-333-894-1	Sequence 1, App1	375	17.2	0.7	42	1	US-08-464-136-75	Sequence 75, App1
C 303	17.2	0.7	42	1	US-08-391-000-36	Sequence 36, App1	376	17.2	0.7	42	2	US-08-349-131-75	Sequence 75, App1
C 304	17.2	0.7	42	2	US-08-741-931-36	Sequence 36, App1	377	17.2	0.7	42	2	US-08-975-902-10	Sequence 10, App1
C 305	17.2	0.7	42	2	US-08-612-858-37	Sequence 37, App1	378	17.2	0.7	42	2	US-08-053-451B-91	Sequence 91, App1
C 306	17.2	0.7	43	2	US-08-756-506-19	Sequence 19, App1	379	17.2	0.7	42	3	US-08-470-297A-75	Sequence 75, App1
C 307	17.2	0.7	43	2	US-08-676-279-11	Sequence 11, App1	380	17.2	0.7	42	3	US-09-251-565-10	Sequence 10, App1
C 308	17.2	0.7	46	2	US-08-452-242-21	Sequence 21, App1	381	17.2	0.7	42	3	US-09-193-191-12	Sequence 12, App1
C 309	17.2	0.7	46	3	US-08-453-176A-21	Sequence 21, App1	382	17.2	0.7	42	4	US-09-138-277C-6	Sequence 6, App1
C 310	17.2	0.7	46	3	US-08-451-374-21	Sequence 21, App1	383	17.2	0.7	42	4	US-09-359-304B-23	Sequence 23, App1
C 311	17.2	0.7	46	4	US-08-935-268A-21	Sequence 21, App1	384	17.2	0.7	42	5	PCT-US91-07149-75	Sequence 75, App1
C 312	17.2	0.7	46	4	US-08-452-229-21	Sequence 21, App1	385	17.2	0.7	43	1	US-07-885-688A-4	Sequence 4, App1
C 313	17.2	0.7	47	4	US-09-360-237-52	Sequence 52, App1	386	17.2	0.7	44	3	US-08-726-807B-28	Sequence 28, App1
C 314	17.2	0.7	47	4	US-09-641-638-1248	Sequence 1248, App	387	17.2	0.7	44	3	US-08-726-807B-41	Sequence 41, App1
C 315	17.2	0.7	48	1	US-08-319-836B-15	Sequence 15, App1	388	17.2	0.7	44	3	US-09-258-367-28	Sequence 28, App1
C 316	17.2	0.7	48	5	PCT-US95-13142-15	Sequence 15, App1	389	17.2	0.7	44	3	US-09-258-367-41	Sequence 41, App1
C 317	17.2	0.7	49	1	US-08-115-497-5	Sequence 5, App1	390	17.2	0.7	44	4	US-09-546-550-28	Sequence 28, App1
C 318	17.2	0.7	49	1	US-08-242-403A-21	Sequence 21, App1	391	17.2	0.7	44	4	US-09-546-550-41	Sequence 41, App1
C 319	17.2	0.7	49	1	US-08-774-128-21	Sequence 21, App1	392	17.2	0.7	44	4	US-09-431-414-28	Sequence 28, App1

C 393	17	0.7	44	4	US-09-431-414-41	Sequence 41, Appl	C 466	16.8	0.7	36	1	US-08-197-791-23	Sequence 23, Appl
C 394	17	0.7	44	4	US-09-225-670-28	Sequence 28, Appl	C 467	16.8	0.7	36	1	US-08-411-795B-410	Sequence 410, Appl
C 395	17	0.7	44	4	US-09-225-670-41	Sequence 41, Appl	C 468	16.8	0.7	36	1	US-08-469-312A-410	Sequence 410, Appl
C 396	17	0.7	44	4	US-09-431-349C-28	Sequence 28, Appl	C 469	16.8	0.7	36	2	US-08-124-981A-7	Sequence 7, Appl
C 397	17	0.7	44	4	US-09-431-349C-41	Sequence 41, Appl	C 470	16.8	0.7	36	3	US-09-037-190-5	Sequence 5, Appl
C 398	17	0.7	45	1	US-08-145-681-9	Sequence 9, Appl	C 471	16.8	0.7	36	3	US-09-037-192-5	Sequence 5, Appl
C 399	17	0.7	45	1	US-08-483-415-24	Sequence 24, Appl	C 472	16.8	0.7	36	3	US-08-833-167-12	Sequence 12, Appl
C 400	17	0.7	45	2	US-08-456-106-9	Sequence 9, Appl	C 473	16.8	0.7	36	3	US-09-037-143-5	Sequence 5, Appl
C 401	17	0.7	45	2	US-08-456-106-9	Sequence 9, Appl	C 474	16.8	0.7	36	3	US-09-049-691-5	Sequence 5, Appl
C 402	17	0.7	45	3	US-08-961-083-235	Sequence 235, Appl	C 475	16.8	0.7	36	4	US-08-260-174-5	Sequence 5, Appl
C 403	17	0.7	45	4	US-09-265-577-9	Sequence 9, Appl	C 476	16.8	0.7	36	4	US-09-338-128A-5	Sequence 5, Appl
C 404	17	0.7	45	4	US-09-627-216A-3	Sequence 3, Appl	C 477	16.8	0.7	36	4	US-09-232-346-5	Sequence 5, Appl
C 405	17	0.7	45	6	5487983-21	Patent No. 5487983	C 478	16.8	0.7	36	4	US-09-344-837A-12	Sequence 5, Appl
C 406	17	0.7	46	1	US-08-171-389-287	Sequence 287, Appl	C 479	16.8	0.7	36	4	US-09-383-143A-44	Sequence 44, Appl
C 407	17	0.7	46	1	US-08-123-936-287	Sequence 287, Appl	C 480	16.8	0.7	36	4	US-09-037-192-5	Sequence 42, Appl
C 408	17	0.7	46	2	US-08-475-228A-287	Sequence 287, Appl	C 481	16.8	0.7	36	4	US-08-764-114-410	Sequence 410, Appl
C 409	17	0.7	46	2	US-08-482-080A-287	Sequence 287, Appl	C 482	16.8	0.7	36	4	US-08-469-419-410	Sequence 410, Appl
C 410	17	0.7	46	3	US-08-961-810-93	Sequence 93, Appl	C 483	16.8	0.7	37	4	US-09-030-156-3	Sequence 410, Appl
C 411	17	0.7	46	4	US-08-352-902D-93	Sequence 287, Appl	C 484	16.8	0.7	37	4	US-09-645-757-3	Sequence 3, Appl
C 412	17	0.7	46	4	US-09-641-638-892	Sequence 892, Appl	C 485	16.8	0.7	38	1	US-08-373-128A-2118	Sequence 3, Appl
C 413	17	0.7	46	4	US-09-641-638-1207	Sequence 1207, Ap	C 486	16.8	0.7	38	1	US-08-435-628-2118	Sequence 2118, Ap
C 414	17	0.7	46	4	US-07-854-603-21	Sequence 1230, Ap	C 487	16.8	0.7	38	4	US-09-031-563-10	Sequence 10, Appl
C 415	17	0.7	46	5	US-08-105-483-102	Sequence 21, Appl	C 488	16.8	0.7	39	1	US-08-418-123A-18	Sequence 18, Appl
C 416	17	0.7	46	5	US-08-936-387-8	Sequence 102, Appl	C 489	16.8	0.7	39	3	US-08-801-154-11	Sequence 11, Appl
C 417	17	0.7	47	2	US-08-641-638-892	Sequence 8, Appl	C 490	16.8	0.7	39	4	US-09-437-032B-19	Sequence 11, Appl
C 418	17	0.7	47	4	US-09-641-638-1207	Sequence 1207, Ap	C 491	16.8	0.7	39	4	US-09-316-083-30	Sequence 30, Appl
C 419	17	0.7	48	1	US-07-854-603-21	Sequence 23, Appl	C 492	16.8	0.7	39	4	US-09-316-083-30	Sequence 43, Appl
C 420	17	0.7	48	1	US-07-854-603-21	Sequence 102, Appl	C 493	16.8	0.7	39	4	US-09-082-649B-43	Sequence 9, Appl
C 421	17	0.7	48	1	US-08-105-483-102	Sequence 102, Appl	C 494	16.8	0.7	39	6	5281520-32	Sequence 9, Appl
C 422	17	0.7	49	1	US-08-105-483-103	Sequence 103, Appl	C 495	16.8	0.7	40	3	US-08-874-825-9	Sequence 25, Appl
C 423	17	0.7	49	1	US-08-207-901-60	Sequence 103, Appl	C 496	16.8	0.7	40	3	US-08-874-825-25	Sequence 9, Appl
C 424	17	0.7	49	1	US-08-709-209-103	Sequence 102, Appl	C 497	16.8	0.7	40	3	US-08-663-824-9	Sequence 25, Appl
C 425	17	0.7	49	1	US-08-709-209-103	Sequence 103, Appl	C 498	16.8	0.7	40	3	US-08-663-824-25	Sequence 25, Appl
C 426	17	0.7	49	1	US-08-257-073-112	Sequence 112, Appl	C 499	16.8	0.7	40	3	US-08-663-824-25	Sequence 25, Appl
C 427	17	0.7	49	1	US-08-458-101-103	Sequence 102, Appl	C 500	16.8	0.7	40	4	US-09-231-303-9	Sequence 25, Appl
C 428	17	0.7	49	1	US-08-458-101-103	Sequence 103, Appl	C 501	16.8	0.7	40	4	US-09-231-303-25	Sequence 25, Appl
C 429	17	0.7	49	2	US-08-801-898A-29	Sequence 11, Appl	C 502	16.8	0.7	41	1	US-07-860-468-14	Sequence 14, Appl
C 430	17	0.7	49	4	US-09-091-814-111	Sequence 111, Appl	C 503	16.8	0.7	41	1	US-07-860-468-15	Sequence 15, Appl
C 431	17	0.7	49	4	US-08-171-389-383	Sequence 383, Appl	C 504	16.8	0.7	42	1	US-07-714-131C-284	Sequence 284, Appl
C 432	17	0.7	50	1	US-08-171-389-383	Sequence 383, Appl	C 505	16.8	0.7	42	1	US-08-412-110-284	Sequence 284, Appl
C 433	17	0.7	50	1	US-08-123-936-383	Sequence 468, Appl	C 506	16.8	0.7	42	1	US-08-409-442A-284	Sequence 284, Appl
C 434	17	0.7	50	1	US-08-123-936-383	Sequence 468, Appl	C 507	16.8	0.7	42	1	US-08-455-633A-11	Sequence 11, Appl
C 435	17	0.7	50	2	US-08-190-109A-4	Sequence 4, Appl	C 508	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, Appl
C 436	17	0.7	50	2	US-08-475-228A-383	Sequence 383, Appl	C 509	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, Appl
C 437	17	0.7	50	2	US-08-475-228A-383	Sequence 383, Appl	C 510	16.8	0.7	42	3	US-09-143-190-284	Sequence 11, Appl
C 438	17	0.7	50	2	US-08-475-228A-383	Sequence 468, Appl	C 511	16.8	0.7	42	3	US-09-502-344-284	Sequence 284, Appl
C 439	17	0.7	50	3	US-08-482-080A-383	Sequence 468, Appl	C 512	16.8	0.7	42	4	US-09-198-119C-29	Sequence 29, Appl
C 440	17	0.7	50	3	US-08-482-080A-383	Sequence 468, Appl	C 513	16.8	0.7	42	4	US-09-225-322B-13	Sequence 13, Appl
C 441	17	0.7	50	3	US-08-985-162-1688	Sequence 1688, Ap	C 514	16.8	0.7	42	5	US-09-454-680-7	Sequence 7, Appl
C 442	17	0.7	50	3	US-08-985-162-1688	Sequence 1719, Ap	C 515	16.8	0.7	43	1	US-08-454-680-7	Sequence 7, Appl
C 443	17	0.7	50	4	US-09-354-947-468	Sequence 383, Appl	C 516	16.8	0.7	43	1	US-08-403-762A-24	Sequence 24, Appl
C 444	17	0.7	50	4	US-09-354-947-468	Sequence 383, Appl	C 517	16.8	0.7	43	1	US-08-403-762A-24	Sequence 24, Appl
C 445	17	0.7	50	4	US-09-354-947-468	Sequence 35, Appl	C 518	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 446	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, Appl	C 519	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 447	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 520	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 448	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 521	16.8	0.7	43	2	US-08-454-680-7	Sequence 7, Appl
C 449	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 522	16.8	0.7	43	2	US-08-454-680-7	Sequence 7, Appl
C 450	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 523	16.8	0.7	43	2	US-08-454-680-7	Sequence 7, Appl
C 451	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 524	16.8	0.7	43	2	US-08-454-680-7	Sequence 7, Appl
C 452	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 525	16.8	0.7	43	2	US-08-454-680-7	Sequence 7, Appl
C 453	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 526	16.8	0.7	43	3	US-08-673-799C-22	Sequence 22, Appl
C 454	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 527	16.8	0.7	43	3	US-08-673-799C-22	Sequence 22, Appl
C 455	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 528	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 456	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 529	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 457	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 530	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 458	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 531	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 459	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 532	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 460	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 533	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 461	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 534	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 462	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 535	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 463	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 536	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 464	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 537	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl
C 465	17	0.7	50	5	PCT-US93-12388-383	Sequence 468, Appl	C 538	16.8	0.7	43	4	US-08-673-799C-22	Sequence 22, Appl

C 539	16.8	0.7	45	4	US-08-976-183A-26	Sequence 26, Appl	612	16.6	0.7	40	4	US-09-306-998-25	Sequence 25, Appl
540	16.8	0.7	45	4	US-08-764-114-171	Sequence 171, App	C 613	16.6	0.7	40	4	US-09-225-645-11	Sequence 11, Appl
541	16.8	0.7	45	4	US-08-469-419-171	Sequence 171, App	C 614	16.6	0.7	40	4	US-09-225-645-17	Sequence 17, Appl
542	16.8	0.7	46	1	US-08-599-252-78	Sequence 78, Appl	C 615	16.6	0.7	40	4	US-08-887-534A-103	Sequence 103, App
543	16.8	0.7	46	1	US-08-436-074-51	Sequence 51, Appl	C 616	16.6	0.7	41	1	US-08-168-917-9	Sequence 9, Appl1
544	16.8	0.7	46	5	PCT-US96-06352-78	Sequence 78, Appl	C 617	16.6	0.7	41	1	US-08-244-722-3	Sequence 9, Appl1
545	16.8	0.7	46	5	PCT-US96-06583-78	Sequence 78, Appl	C 618	16.6	0.7	41	2	US-08-460-510-9	Sequence 9, Appl1
546	16.8	0.7	47	2	US-08-936-387-9	Sequence 9, Appl1	C 619	16.6	0.7	41	1	US-08-460-490-9	Sequence 9, Appl1
547	16.8	0.7	47	3	US-08-464-582-8	Sequence 8, Appl1	C 620	16.6	0.7	41	5	US-09-035-665-7	Sequence 7, Appl1
548	16.8	0.7	47	3	US-08-464-582-9	Sequence 9, Appl1	C 621	16.6	0.7	41	5	PCT-US92-00730-9	Sequence 9, Appl1
549	16.8	0.7	47	4	US-08-462-513-8	Sequence 8, Appl1	C 622	16.6	0.7	41	5	PCT-US92-10430-4	Sequence 4, Appl1
550	16.8	0.7	47	4	US-08-462-513-9	Sequence 9, Appl1	C 623	16.6	0.7	42	1	US-08-464-531-64	Sequence 64, Appl1
551	16.8	0.7	47	4	US-09-641-638-748	Sequence 748, App	C 624	16.6	0.7	42	1	US-08-487-037-8	Sequence 8, Appl1
552	16.8	0.7	47	4	US-09-641-638-759	Sequence 759, App	C 625	16.6	0.7	42	2	US-08-461-598-64	Sequence 64, Appl
553	16.8	0.7	47	4	US-09-641-638-1237	Sequence 1237, App	C 626	16.6	0.7	42	2	US-08-053-451B-89	Sequence 89, Appl
554	16.8	0.7	48	1	US-08-602-036A-12	Sequence 12, Appl	C 627	16.6	0.7	42	3	US-08-332-137-64	Sequence 64, Appl
555	16.8	0.7	48	1	US-08-389-459A-14	Sequence 14, Appl	C 628	16.6	0.7	42	3	US-08-336-632B-20	Sequence 20, Appl
556	16.8	0.7	48	2	US-08-502-374A-12	Sequence 12, Appl	C 629	16.6	0.7	42	4	US-09-042-353-380	Sequence 380, App
557	16.8	0.7	48	2	US-08-642-407A-12	Sequence 12, Appl	C 630	16.6	0.7	42	4	US-09-042-353-380	Sequence 23, Appl
558	16.8	0.7	50	1	US-08-987-867A-14	Sequence 14, Appl	C 631	16.6	0.7	44	1	US-07-872-673B-230	Sequence 12, Appl
559	16.8	0.7	50	1	US-08-123-936-379	Sequence 379, App	C 632	16.6	0.7	44	1	US-08-681-935-12	Sequence 35, Appl
560	16.8	0.7	50	1	US-08-123-936-379	Sequence 379, App	C 633	16.6	0.7	44	1	US-08-741-881-35	Sequence 35, Appl
561	16.8	0.7	50	1	US-08-374-641-36	Sequence 36, Appl	C 634	16.6	0.7	44	1	US-08-739-158-35	Sequence 35, Appl
562	16.8	0.7	50	2	US-08-475-228A-379	Sequence 379, App	C 635	16.6	0.7	44	1	US-08-739-167-35	Sequence 35, Appl
563	16.8	0.7	50	3	US-08-482-080A-379	Sequence 379, App	C 636	16.6	0.7	44	2	US-08-404-796-35	Sequence 35, Appl
564	16.8	0.7	50	3	US-08-985-162-1727	Sequence 1727, App	C 637	16.6	0.7	44	3	US-08-931-869-35	Sequence 35, Appl
565	16.8	0.7	50	4	US-08-849-567A-66	Sequence 66, Appl	C 638	16.6	0.7	44	3	US-08-939-323-132	Sequence 12, Appl
566	16.8	0.7	50	4	US-09-354-947-379	Sequence 379, App	C 639	16.6	0.7	44	4	US-09-350-399-35	Sequence 35, Appl
567	16.8	0.7	50	5	PCT-US93-12388-379	Sequence 379, App	C 640	16.6	0.7	44	4	US-09-236-140A-35	Sequence 35, Appl
568	16.8	0.7	24	1	US-08-435-529-7	Sequence 7, Appl1	C 641	16.6	0.7	44	4	US-09-415-784-58	Sequence 58, Appl
569	16.6	0.7	25	3	US-08-810-720-3	Sequence 3, Appl1	C 642	16.6	0.7	44	4	US-09-415-785A-58	Sequence 58, Appl
570	16.6	0.7	27	4	US-09-253-396A-10	Sequence 10, Appl1	C 643	16.6	0.7	44	4	US-08-944-465-58	Sequence 58, Appl
571	16.6	0.7	27	4	US-08-584-040-158	Sequence 158, App	C 644	16.6	0.7	44	4	US-09-415-868-58	Sequence 58, Appl
572	16.6	0.7	32	1	US-08-442-542-48	Sequence 48, Appl	C 645	16.6	0.7	44	4	US-09-415-900-58	Sequence 58, Appl
573	16.6	0.7	32	3	US-08-974-180-27	Sequence 27, Appl	C 646	16.6	0.7	44	6	5242821-25	Patent No. 5242821
574	16.6	0.7	32	3	US-08-765-469-48	Sequence 48, Appl	C 647	16.6	0.7	44	3	US-08-329-799-72	Sequence 72, Appl
575	16.6	0.7	33	3	US-08-364-339-19	Sequence 19, Appl	C 648	16.6	0.7	45	3	US-08-834-314-2	Sequence 2, Appl1
576	16.6	0.7	33	1	US-08-413-118-114	Sequence 114, App	C 649	16.6	0.7	45	5	PCT-US96-00888-14	Sequence 14, Appl
577	16.6	0.7	33	1	US-08-487-034-19	Sequence 19, Appl	C 650	16.6	0.7	45	5	US-09-641-638-1292	Sequence 1292, App
578	16.6	0.7	33	2	US-08-975-902-46	Sequence 46, Appl	C 651	16.6	0.7	46	4	US-08-616-387-8	Sequence 8, Appl1
579	16.6	0.7	33	2	US-08-360-606B-14	Sequence 14, Appl	C 652	16.6	0.7	47	2	US-08-883-795A-29	Sequence 29, Appl
580	16.6	0.7	33	3	US-08-577-121-26	Sequence 26, Appl	C 653	16.6	0.7	47	2	US-08-883-795A-30	Sequence 30, Appl
581	16.6	0.7	33	3	US-08-473-446-114	Sequence 114, App	C 654	16.6	0.7	47	2	US-09-338-907-324	Sequence 324, App
582	16.6	0.7	33	3	US-08-810-720-4	Sequence 4, Appl1	C 655	16.6	0.7	47	4	US-09-218-207-424	Sequence 38, Appl
583	16.6	0.7	33	3	US-09-251-565-46	Sequence 46, Appl	C 656	16.6	0.7	47	4	US-09-345-882-38	Sequence 743, App
584	16.6	0.7	33	4	US-08-985-700-26	Sequence 26, Appl	C 657	16.6	0.7	47	4	US-09-641-638-743	Sequence 1032, App
585	16.6	0.7	33	4	US-09-411-977-29	Sequence 29, Appl	C 658	16.6	0.7	47	4	US-09-641-638-1032	Sequence 1079, App
586	16.6	0.7	33	5	PCT-US95-16916-26	Sequence 26, Appl	C 659	16.6	0.7	47	4	US-09-641-638-1079	Sequence 1152, App
587	16.6	0.7	34	1	US-08-270-985-18	Sequence 18, Appl	C 660	16.6	0.7	47	4	US-08-616-133-13	Sequence 13, Appl
588	16.6	0.7	34	2	US-08-479-733A-19	Sequence 19, Appl	C 661	16.6	0.7	47	4	US-08-802-985-13	Sequence 40, Appl
589	16.6	0.7	34	3	US-08-487-427-19	Sequence 19, Appl	C 662	16.6	0.7	48	1	US-08-975-902-40	Sequence 16, Appl
590	16.6	0.7	34	3	US-08-479-727A-19	Sequence 19, Appl	C 663	16.6	0.7	48	2	US-08-845-161A-16	Sequence 16, Appl
591	16.6	0.7	34	3	US-08-478-208-27	Sequence 27, Appl	C 664	16.6	0.7	48	2	US-09-251-565-50	Sequence 40, Appl
592	16.6	0.7	34	3	US-08-482-369A-19	Sequence 19, Appl	C 665	16.6	0.7	48	2	US-09-270-751-16	Sequence 16, Appl
593	16.6	0.7	34	3	US-09-009-217-25	Sequence 25, Appl	C 666	16.6	0.7	48	4	US-09-305-408-9	Sequence 9, Appl1
594	16.6	0.7	34	3	US-09-009-656-25	Sequence 25, Appl	C 667	16.6	0.7	48	4	US-08-692-610-9	Sequence 9, Appl1
595	16.6	0.7	34	5	PCT-US95-07439-19	Sequence 19, Appl	C 668	16.6	0.7	49	1	US-08-682-471-8	Sequence 8, Appl1
596	16.6	0.7	35	4	US-09-386-607-8	Sequence 8, Appl1	C 669	16.6	0.7	49	1	US-08-683-124-9	Sequence 9, Appl1
597	16.6	0.7	35	4	US-08-235-836C-25	Sequence 25, Appl	C 670	16.6	0.7	49	1	US-09-538-709-1177	Sequence 1177, App
598	16.6	0.7	36	2	US-08-669-721-1	Sequence 1, Appl1	C 671	16.6	0.7	49	1	US-08-171-389-562	Sequence 562, App
599	16.6	0.7	36	2	US-08-140-083A-4	Sequence 195, App	C 672	16.6	0.7	50	1	US-08-120-901-41	Sequence 41, Appl
600	16.6	0.7	36	3	US-08-781-891-195	Sequence 1, Appl1	C 673	16.6	0.7	50	1	US-08-120-936-562	Sequence 562, App
601	16.6	0.7	36	4	US-09-189-344-1	Sequence 9, Appl1	C 674	16.6	0.7	50	1	US-08-475-228A-562	Sequence 562, App
602	16.6	0.7	37	1	US-08-387-315A-9	Sequence 9, Appl1	C 675	16.6	0.7	50	2	US-08-482-080A-562	Sequence 562, App
603	16.6	0.7	37	2	US-08-754-559-9	Sequence 2, Appl1	C 676	16.6	0.7	50	4	US-09-354-947-562	Sequence 562, App
604	16.6	0.7	38	4	US-09-054-711C-2	Sequence 60, Appl	C 677	16.6	0.7	50	4	PCT-US93-12388-562	Sequence 562, App
605	16.6	0.7	39	1	US-08-634-060-60	Sequence 8, Appl1	C 678	16.6	0.7	50	4	US-09-489-765A-36	Sequence 36, App
606	16.6	0.7	39	4	US-09-292-563-8	Sequence 112, App	C 679	16.6	0.7	20	4	US-08-060-925A-7	Sequence 7, Appl1
607	16.6	0.7	39	4	US-09-564-805-112	Patent No. 5256648	C 680	16.4	0.7	26	1	US-08-758-306-724	Sequence 74, Appl
608	16.6	0.7	39	6	5256648-29	Sequence 11, Appl	C 681	16.4	0.7	27	1	US-08-758-306-724	Sequence 1120, App
609	16.6	0.7	40	2	US-08-281-423-11	Sequence 17, Appl	C 682	16.4	0.7	27	1		
610	16.6	0.7	40	2	US-08-281-423-17	Sequence 16, Appl	C 683	16.4	0.7	27	1		
611	16.6	0.7	40	4	US-08-748-547-16	Sequence 16, Appl	C 684	16.4	0.7	27	1		

C 685	16.4	0.7	27	3	US-08-985-162-1312	Sequence 1312, Ap	C 758	16.4	0.7	42	3	US-08-612-973-103	Sequence 103, App
686	16.4	0.7	27	3	US-08-985-162-1315	Sequence 1315, Ap	C 759	16.4	0.7	42	4	US-08-927-597-103	Sequence 103, App
687	16.4	0.7	27	4	US-08-584-040-192	Sequence 192, App	C 760	16.4	0.7	42	4	US-08-813-781-43	Sequence 43, App1
C 688	16.4	0.7	27	4	US-08-584-040-622	Sequence 622, App	C 761	16.4	0.7	42	5	PCT-US95-12414-8	Sequence 8, App1
C 689	16.4	0.7	27	4	US-08-584-040-1046	Sequence 1046, Ap	C 762	16.4	0.7	43	1	US-08-403-762a-18	Sequence 18, App1
C 690	16.4	0.7	30	2	US-08-632-470-16	Sequence 16, App1	C 763	16.4	0.7	43	1	US-08-403-762a-20	Sequence 20, App1
C 691	16.4	0.7	31	1	US-08-647-584-44	Sequence 44, App1	C 764	16.4	0.7	43	1	US-08-292-081a-13	Sequence 13, App1
692	16.4	0.7	33	4	US-09-191-852-10	Sequence 10, App1	C 765	16.4	0.7	43	2	US-08-752-495-13	Sequence 13, App1
693	16.4	0.7	33	5	US-08-817-906-10	Sequence 10, App1	C 766	16.4	0.7	43	4	US-09-387-800-5	Sequence 5, App1
694	16.4	0.7	33	5	PCT-US95-13376-10	Sequence 10, App1	C 767	16.4	0.7	43	4	US-09-363-939a-91	Sequence 91, App1
695	16.4	0.7	35	1	US-08-126-594-15	Sequence 15, App1	C 768	16.4	0.7	44	1	US-07-931-473b-110	Sequence 110, App
696	16.4	0.7	35	1	US-08-126-594-17	Sequence 17, App1	C 769	16.4	0.7	44	1	US-07-714-131c-110	Sequence 110, App
697	16.4	0.7	35	1	US-08-126-594-19	Sequence 19, App1	C 770	16.4	0.7	44	1	US-08-458-084-17	Sequence 17, App1
698	16.4	0.7	35	1	US-08-048-975-3	Sequence 3, App1	C 771	16.4	0.7	44	1	US-08-205-508-17	Sequence 17, App1
699	16.4	0.7	35	1	US-08-364-339-16	Sequence 16, App1	C 772	16.4	0.7	44	1	US-08-412-110-110	Sequence 110, App
700	16.4	0.7	35	1	US-08-465-811a-15	Sequence 15, App1	C 773	16.4	0.7	44	1	US-08-409-442a-110	Sequence 110, App
701	16.4	0.7	35	1	US-08-465-811a-17	Sequence 17, App1	C 774	16.4	0.7	44	2	US-08-469-609a-110	Sequence 110, App
702	16.4	0.7	35	1	US-08-487-034-16	Sequence 16, App1	C 775	16.4	0.7	44	3	US-09-143-190-110	Sequence 110, App
703	16.4	0.7	35	2	US-08-619-542b-15	Sequence 15, App1	C 776	16.4	0.7	44	4	US-09-502-344-110	Sequence 110, App
704	16.4	0.7	35	2	US-08-619-542b-17	Sequence 17, App1	C 777	16.4	0.7	44	5	PCT-US95-02945-17	Sequence 17, App1
705	16.4	0.7	35	2	US-08-619-542b-19	Sequence 19, App1	C 778	16.4	0.7	45	1	US-07-885-689a-10	Sequence 10, App1
706	16.4	0.7	35	2	US-08-479-733a-6	Sequence 6, App1	C 779	16.4	0.7	45	1	US-08-219-242a-4	Sequence 4, App1
C 707	16.4	0.7	35	2	US-08-479-733a-6	Sequence 6, App1	C 780	16.4	0.7	45	1	US-08-197-770-6	Sequence 6, App1
708	16.4	0.7	35	2	US-08-405-373c-2	Sequence 2, App1	C 781	16.4	0.7	45	1	US-08-197-770-8	Sequence 8, App1
709	16.4	0.7	35	3	US-08-577-121-23	Sequence 23, App1	C 782	16.4	0.7	45	1	US-08-171-389-61	Sequence 61, App1
C 710	16.4	0.7	35	3	US-08-487-427-6	Sequence 6, App1	C 783	16.4	0.7	45	1	US-08-148-022-2	Sequence 2, App1
C 711	16.4	0.7	35	3	US-08-479-727a-6	Sequence 6, App1	C 784	16.4	0.7	45	1	US-08-476-685d-4	Sequence 4, App1
C 712	16.4	0.7	35	3	US-08-482-369a-6	Sequence 6, App1	C 785	16.4	0.7	45	1	US-07-854-603-31	Sequence 31, App1
C 713	16.4	0.7	35	4	US-08-985-700-23	Sequence 23, App1	C 786	16.4	0.7	45	1	US-08-472-877b-4	Sequence 4, App1
C 714	16.4	0.7	35	4	US-09-168-738a-26	Sequence 26, App1	C 787	16.4	0.7	45	1	US-08-451-822a-10	Sequence 10, App1
C 715	16.4	0.7	35	4	US-09-940-019-26	Sequence 26, App1	C 788	16.4	0.7	45	2	US-08-475-828a-61	Sequence 61, App1
C 716	16.4	0.7	35	5	PCT-US95-07439-6	Sequence 6, App1	C 789	16.4	0.7	45	3	US-08-482-080a-61	Sequence 61, App1
717	16.4	0.7	35	5	PCT-US95-16916-23	Sequence 23, App1	C 790	16.4	0.7	45	4	US-09-072-958-4	Sequence 4, App1
718	16.4	0.7	36	2	US-08-292-620a-1382	Sequence 1382, Ap	C 791	16.4	0.7	45	4	US-08-323-430-10	Sequence 10, App1
719	16.4	0.7	36	2	US-08-292-620a-1444	Sequence 1444, Ap	C 792	16.4	0.7	45	4	US-09-293-505-21	Sequence 21, App1
720	16.4	0.7	36	2	US-08-471-371-3	Sequence 3, App1	C 793	16.4	0.7	45	4	US-09-354-947-61	Sequence 61, App1
721	16.4	0.7	36	3	US-08-444-644-13	Sequence 13, App1	C 794	16.4	0.7	45	4	US-09-517-871-15	Sequence 15, App1
722	16.4	0.7	36	3	US-09-071-845-1382	Sequence 1382, Ap	C 795	16.4	0.7	45	5	PCT-US93-12388-61	Sequence 61, App1
723	16.4	0.7	36	3	US-09-071-845-1444	Sequence 1444, Ap	C 796	16.4	0.7	45	5	PCT-US95-14639-8	Sequence 8, App1
C 724	16.4	0.7	36	4	US-08-358-627f-24	Sequence 24, App1	C 797	16.4	0.7	45	5	US-08-663-688a-4	Sequence 4, App1
725	16.4	0.7	36	4	US-08-450-962-9	Sequence 9, App1	C 798	16.4	0.7	46	2	US-08-191-160-25	Sequence 25, App1
C 726	16.4	0.7	36	4	US-08-332-245a-13	Sequence 13, App1	C 799	16.4	0.7	46	4	US-08-639-763-11	Sequence 11, App1
C 727	16.4	0.7	36	4	US-09-219-797-5	Sequence 5, App1	C 800	16.4	0.7	47	2	US-08-783-275-6	Sequence 6, App1
C 728	16.4	0.7	36	4	US-08-465-712c-24	Sequence 24, App1	C 801	16.4	0.7	47	4	US-08-727-708-6	Sequence 6, App1
C 729	16.4	0.7	36	4	US-09-552-733-24	Sequence 24, App1	C 802	16.4	0.7	47	4	US-08-383-621-8	Sequence 8, App1
C 730	16.4	0.7	38	4	US-09-262-773-45	Sequence 45, App1	C 803	16.4	0.7	47	4	US-08-459-906-8	Sequence 8, App1
C 731	16.4	0.7	38	4	US-08-469-260a-146	Sequence 146, App	C 804	16.4	0.7	47	4	US-08-789-333b-66	Sequence 66, App1
C 732	16.4	0.7	39	1	US-07-931-473b-146	Sequence 146, App	C 805	16.4	0.7	47	4	US-08-789-333b-101	Sequence 101, App1
C 733	16.4	0.7	39	1	US-08-412-110-146	Sequence 110, App	C 806	16.4	0.7	47	4	US-09-367-206-9	Sequence 9, App1
C 734	16.4	0.7	39	1	US-08-409-442a-146	Sequence 146, App	C 807	16.4	0.7	47	4	US-08-887-983-30	Sequence 30, App1
C 735	16.4	0.7	39	1	US-08-409-442a-146	Sequence 146, App	C 808	16.4	0.7	47	4	US-08-588-976-30	Sequence 30, App1
C 736	16.4	0.7	39	2	US-08-469-609a-146	Sequence 146, App	C 809	16.4	0.7	48	4	US-09-400-541-10	Sequence 10, App1
C 737	16.4	0.7	39	3	US-09-235-246-17	Sequence 17, App1	C 810	16.4	0.7	48	4	US-08-899-999-10	Sequence 10, App1
C 738	16.4	0.7	39	3	US-09-143-190-146	Sequence 146, App	C 811	16.4	0.7	48	4	US-08-171-389-378	Sequence 378, App
C 739	16.4	0.7	39	4	US-09-502-344-146	Sequence 146, App	C 812	16.4	0.7	48	4	US-08-324-001-10	Sequence 10, App1
C 740	16.4	0.7	39	4	US-09-517-871-16	Sequence 16, App	C 813	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
741	16.4	0.7	40	1	US-08-199-507b-46	Sequence 46, App1	C 814	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
742	16.4	0.7	40	1	US-08-441-828-46	Sequence 46, App1	C 815	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
C 743	16.4	0.7	40	1	US-08-040-548-58	Sequence 58, App1	C 816	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
C 744	16.4	0.7	40	1	US-08-466-344-58	Sequence 58, App1	C 817	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
C 745	16.4	0.7	40	2	US-08-867-941-61	Sequence 61, App1	C 818	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
C 746	16.4	0.7	40	2	US-09-074-658-61	Sequence 61, App1	C 819	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
747	16.4	0.7	40	4	US-09-313-221a-71	Sequence 71, App1	C 820	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
748	16.4	0.7	41	1	US-08-357-698-2	Sequence 2, App1	C 821	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
749	16.4	0.7	41	2	US-08-822-701-16	Sequence 16, App1	C 822	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
750	16.4	0.7	41	5	US-08-935-855-16	Sequence 16, App1	C 823	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
751	16.4	0.7	41	5	PCT-US93-12682-2	Sequence 2, App1	C 824	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
752	16.4	0.7	42	1	US-08-466-603-8	Sequence 8, App1	C 825	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
753	16.4	0.7	42	1	US-08-314-503a-8	Sequence 8, App1	C 826	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
754	16.4	0.7	42	1	US-08-468-066-8	Sequence 8, App1	C 827	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
755	16.4	0.7	42	2	US-08-466-717-8	Sequence 8, App1	C 828	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
756	16.4	0.7	42	3	US-08-836-337-1	Sequence 1, App1	C 829	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1
757	16.4	0.7	42	3	US-08-466-743-8	Sequence 8, App1	C 830	16.4	0.7	48	6	US-08-324-001-11	Sequence 11, App1

C 831	16.4	0.7	50	1	US-08-471-206-26	Sequence 26, Appl	C 904	16.2	0.7	38	2	US-08-292-620A-2126	Sequence 2126, Ap
C 832	16.4	0.7	50	1	US-08-123-936-378	Sequence 378, App	C 905	16.2	0.7	38	2	US-08-292-620A-2307	Sequence 2307, Ap
C 833	16.4	0.7	50	1	US-08-123-936-599	Sequence 599, App	C 906	16.2	0.7	38	2	US-08-857-946-51	Sequence 51, Appl
C 834	16.4	0.7	50	2	US-08-828-007-7	Sequence 7, Appl	C 907	16.2	0.7	38	3	US-08-970-740-51	Sequence 51, Appl
C 835	16.4	0.7	50	2	US-08-475-228A-378	Sequence 378, App	C 908	16.2	0.7	38	3	US-09-071-845-2126	Sequence 2126, Ap
C 836	16.4	0.7	50	2	US-08-475-228A-599	Sequence 599, App	C 909	16.2	0.7	38	3	US-09-071-845-2307	Sequence 2307, Ap
C 837	16.4	0.7	50	2	US-08-832-468-2	Sequence 2, Appl	C 910	16.2	0.7	38	4	US-09-232-479-24	Sequence 24, Appl
C 838	16.4	0.7	50	3	US-08-482-080A-378	Sequence 378, App	C 911	16.2	0.7	38	4	US-09-784-990-24	Sequence 24, Appl
C 839	16.4	0.7	50	3	US-08-482-080A-599	Sequence 599, App	C 912	16.2	0.7	39	1	US-08-331-398A-4	Sequence 4, Appl
C 840	16.4	0.7	50	3	US-08-985-162-1669	Sequence 1669, Ap	C 913	16.2	0.7	39	1	US-08-469-665-5	Sequence 5, Appl
C 841	16.4	0.7	50	4	US-09-354-947-378	Sequence 378, App	C 914	16.2	0.7	39	1	US-08-417-210A-58	Sequence 58, Appl
C 842	16.4	0.7	50	4	US-09-354-947-599	Sequence 599, App	C 915	16.2	0.7	39	2	US-09-038-596-5	Sequence 5, Appl
C 843	16.4	0.7	50	5	PCT-US93-12388-378	Sequence 378, App	C 916	16.2	0.7	39	2	US-09-038-596-5	Sequence 5, Appl
C 844	16.4	0.7	50	5	PCT-US93-12388-599	Sequence 599, App	C 917	16.2	0.7	39	2	US-08-331-397B-4	Sequence 4, Appl
C 845	16.2	0.7	24	2	US-08-632-575B-25	Sequence 25, Appl	C 918	16.2	0.7	39	2	US-08-759-804A-4	Sequence 4, Appl
C 846	16.2	0.7	27	1	US-07-910-222B-1	Sequence 1, Appl	C 919	16.2	0.7	39	4	US-09-227-693-3	Sequence 23, Appl
C 847	16.2	0.7	27	1	US-07-910-222B-3	Sequence 3, Appl	C 920	16.2	0.7	39	4	US-08-860-038-23	Sequence 23, Appl
C 848	16.2	0.7	27	1	US-08-070-158-2	Sequence 2, Appl	C 921	16.2	0.7	39	4	US-09-580-923-23	Sequence 23, Appl
C 849	16.2	0.7	27	1	US-08-200-716-1	Sequence 1, Appl	C 922	16.2	0.7	39	5	PCT-US95-00421-5	Sequence 5, Appl
C 850	16.2	0.7	27	1	US-08-200-716-3	Sequence 3, Appl	C 923	16.2	0.7	40	1	US-08-443-957-10	Sequence 10, Appl
C 851	16.2	0.7	27	2	US-08-015-147-1	Sequence 1, Appl	C 924	16.2	0.7	40	4	US-09-091-814-85	Sequence 85, Appl
C 852	16.2	0.7	27	2	US-08-015-147-3	Sequence 3, Appl	C 925	16.2	0.7	40	4	US-09-189-462-25	Sequence 25, Appl
C 853	16.2	0.7	27	2	US-08-482-651-55	Sequence 55, Appl	C 926	16.2	0.7	40	4	US-09-189-462-26	Sequence 26, Appl
C 854	16.2	0.7	27	3	US-08-469-015-2	Sequence 2, Appl	C 927	16.2	0.7	41	1	US-08-480-525-3	Sequence 3, Appl
C 855	16.2	0.7	27	3	US-08-463-893-2	Sequence 2, Appl	C 928	16.2	0.7	41	1	US-08-477-934-28	Sequence 28, Appl
C 856	16.2	0.7	27	4	US-08-660-092-209	Sequence 209, App	C 929	16.2	0.7	41	4	US-07-986-776A-28	Sequence 28, Appl
C 857	16.2	0.7	27	4	US-09-358-972-99	Sequence 99, Appl	C 930	16.2	0.7	41	4	US-09-233-086-47	Sequence 47, Appl
C 858	16.2	0.7	27	4	US-09-504-505-2	Sequence 2, Appl	C 931	16.2	0.7	41	5	US-07-986-776A-28	Sequence 28, Appl
C 859	16.2	0.7	27	4	US-08-980-241-1	Sequence 1, Appl	C 932	16.2	0.7	42	1	PCT-US94-06422-3	Sequence 3, Appl
C 860	16.2	0.7	27	4	US-09-160-513-209	Sequence 209, App	C 933	16.2	0.7	42	1	US-08-391-000-34	Sequence 34, Appl
C 861	16.2	0.7	30	1	US-08-347-792-21	Sequence 21, Appl	C 934	16.2	0.7	42	2	US-08-741-931-34	Sequence 34, Appl
C 862	16.2	0.7	30	1	US-08-431-357-21	Sequence 21, Appl	C 935	16.2	0.7	42	3	US-08-956-047-18	Sequence 18, Appl
C 863	16.2	0.7	30	2	US-08-454-557C-6	Sequence 6, Appl	C 936	16.2	0.7	42	3	US-08-480-640A-120	Sequence 120, App
C 864	16.2	0.7	30	2	US-08-340-426D-6	Sequence 6, Appl	C 937	16.2	0.7	42	3	US-08-962-503-1	Sequence 1, Appl
C 865	16.2	0.7	30	2	US-08-450-673C-6	Sequence 6, Appl	C 938	16.2	0.7	42	4	US-08-295-802-120	Sequence 120, App
C 866	16.2	0.7	30	2	US-08-642-406A-14	Sequence 14, Appl	C 939	16.2	0.7	42	4	US-08-375-992A-120	Sequence 120, App
C 867	16.2	0.7	30	3	US-08-434-000A-16	Sequence 16, Appl	C 940	16.2	0.7	43	1	US-08-473-096-1	Sequence 1, Appl
C 868	16.2	0.7	30	3	US-08-961-083-417	Sequence 417, App	C 941	16.2	0.7	43	3	US-08-934-494-11	Sequence 11, Appl
C 869	16.2	0.7	30	4	US-09-312-157-16	Sequence 16, Appl	C 942	16.2	0.7	43	3	US-09-143-068-11	Sequence 11, Appl
C 870	16.2	0.7	30	4	US-09-199-534-14	Sequence 14, Appl	C 943	16.2	0.7	43	4	US-08-906-156A-81	Sequence 81, Appl
C 871	16.2	0.7	30	4	US-08-956-653A-28	Sequence 28, Appl	C 944	16.2	0.7	43	4	US-09-143-707-11	Sequence 11, Appl
C 872	16.2	0.7	30	4	US-08-327-874A-31	Sequence 31, Appl	C 945	16.2	0.7	43	4	US-09-202-089-11	Sequence 11, Appl
C 873	16.2	0.7	30	4	US-09-199-534-14	Sequence 14, Appl	C 946	16.2	0.7	43	4	US-09-511-133-11	Sequence 11, Appl
C 874	16.2	0.7	30	5	PCT-US94-09700-31	Sequence 31, Appl	C 947	16.2	0.7	43	4	US-09-690-169-11	Sequence 11, Appl
C 875	16.2	0.7	30	5	PCT-US95-15353-21	Sequence 21, Appl	C 948	16.2	0.7	43	4	US-09-511-631-11	Sequence 11, Appl
C 876	16.2	0.7	30	5	PCT-US95-17111A-6	Sequence 6, Appl	C 949	16.2	0.7	44	1	US-08-171-389-2	Sequence 2, Appl
C 877	16.2	0.7	32	1	US-08-239-889A-2	Sequence 2, Appl	C 950	16.2	0.7	44	1	US-08-123-936-2	Sequence 2, Appl
C 878	16.2	0.7	32	2	US-08-889-909A-20	Sequence 20, Appl	C 951	16.2	0.7	44	2	US-08-475-228A-2	Sequence 2, Appl
C 879	16.2	0.7	32	2	US-09-073-395-4	Sequence 4, Appl	C 952	16.2	0.7	44	3	US-08-482-080A-2	Sequence 2, Appl
C 880	16.2	0.7	32	4	US-09-156-163A-20	Sequence 20, Appl	C 953	16.2	0.7	44	4	US-09-354-947-2	Sequence 2, Appl
C 881	16.2	0.7	32	5	PCT-US95-05659-2	Sequence 2, Appl	C 954	16.2	0.7	44	5	PCT-US93-12388-2	Sequence 2, Appl
C 882	16.2	0.7	33	3	US-08-711-218-9	Sequence 9, Appl	C 955	16.2	0.7	45	1	US-08-411-795B-173	Sequence 173, App
C 883	16.2	0.7	33	3	US-08-726-807B-11	Sequence 11, Appl	C 956	16.2	0.7	45	1	US-08-469-319A-173	Sequence 173, App
C 884	16.2	0.7	33	3	US-09-258-367-11	Sequence 11, Appl	C 957	16.2	0.7	45	2	US-08-975-902-33	Sequence 33, Appl
C 885	16.2	0.7	33	3	US-08-454-928-3	Sequence 3, Appl	C 958	16.2	0.7	45	2	US-08-560-098A-25	Sequence 25, Appl
C 886	16.2	0.7	33	4	US-09-546-550-11	Sequence 11, Appl	C 959	16.2	0.7	45	3	US-09-251-365-33	Sequence 33, Appl
C 887	16.2	0.7	33	4	US-09-431-414-11	Sequence 11, Appl	C 960	16.2	0.7	45	4	US-08-764-419-173	Sequence 173, App
C 888	16.2	0.7	33	4	US-09-225-670-11	Sequence 11, Appl	C 961	16.2	0.7	45	4	US-08-469-419-173	Sequence 173, App
C 889	16.2	0.7	33	4	US-09-431-349C-11	Sequence 11, Appl	C 962	16.2	0.7	46	1	US-08-171-389-146	Sequence 146, App
C 890	16.2	0.7	35	1	US-08-361-337-60	Sequence 60, Appl	C 963	16.2	0.7	46	1	US-08-123-936-146	Sequence 146, App
C 891	16.2	0.7	35	1	US-08-399-696-69	Sequence 69, Appl	C 964	16.2	0.7	46	2	US-08-475-228A-146	Sequence 146, App
C 892	16.2	0.7	35	4	US-09-597-877-22	Sequence 22, Appl	C 965	16.2	0.7	46	3	US-08-482-080A-146	Sequence 146, App
C 893	16.2	0.7	36	1	US-08-435-350-19	Sequence 19, Appl	C 966	16.2	0.7	46	4	US-09-406-074-3	Sequence 3, Appl
C 894	16.2	0.7	36	2	US-08-140-083A-3	Sequence 3, Appl	C 967	16.2	0.7	46	4	US-09-354-947-146	Sequence 146, App
C 895	16.2	0.7	36	2	US-08-455-968B-42	Sequence 42, Appl	C 968	16.2	0.7	46	4	US-09-345-882-60	Sequence 60, Appl
C 896	16.2	0.7	36	3	US-08-781-891-198	Sequence 198, App	C 969	16.2	0.7	46	4	US-09-641-638-833	Sequence 833, App
C 897	16.2	0.7	37	1	US-08-264-115-5	Sequence 5, Appl	C 970	16.2	0.7	46	4	US-09-313-221A-16	Sequence 16, Appl
C 898	16.2	0.7	37	1	US-08-387-315A-9	Sequence 9, Appl	C 971	16.2	0.7	46	5	PCT-US93-12388-146	Sequence 146, App
C 899	16.2	0.7	37	1	US-08-294-424-42	Sequence 42, Appl	C 972	16.2	0.7	47	1	US-08-171-389-165	Sequence 165, App
C 900	16.2	0.7	37	2	US-08-754-559-9	Sequence 9, Appl	C 973	16.2	0.7	47	1	US-08-123-936-165	Sequence 165, App
C 901	16.2	0.7	37	2	US-08-398-590A-50	Sequence 50, Appl	C 974	16.2	0.7	47	2	US-08-475-228A-165	Sequence 165, App
C 902	16.2	0.7	37	4	US-08-894-997-52	Sequence 52, Appl	C 975	16.2	0.7	47	2	US-08-553-257A-5	Sequence 5, Appl
C 903	16.2	0.7	38	1	US-08-441-714-2	Sequence 2, Appl	C 976	16.2	0.7	47	3	US-08-482-080A-165	Sequence 165, App

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977 16.2 0.7 47 4 US-09-045-284A-8
C 978 16.2 0.7 47 4 US-09-338-907-210
C 979 16.2 0.7 47 4 US-09-218-207-210
980 16.2 0.7 47 4 US-09-190-911-8
C 981 16.2 0.7 47 4 US-09-354-947-165
C 982 16.2 0.7 47 4 US-09-345-882-48
C 983 16.2 0.7 47 4 US-09-345-882-54
C 984 16.2 0.7 47 4 US-09-641-638-839
C 985 16.2 0.7 47 4 US-09-641-638-840
C 986 16.2 0.7 47 4 US-09-641-638-1167
C 987 16.2 0.7 47 4 US-09-641-638-1219
C 988 16.2 0.7 47 4 US-09-641-638-1231
C 989 16.2 0.7 47 5 PCT-US93-12388-165
C 990 16.2 0.7 47 5 PCT-US94-01149-35
C 991 16.2 0.7 47 5 PCT-US94-01149-64
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C 993 16.2 0.7 48 1 US-08-209-182C-18
C 994 16.2 0.7 48 1 US-08-171-389-19
C 995 16.2 0.7 48 1 US-08-391-000-2
C 996 16.2 0.7 48 1 US-08-123-936-19
C 997 16.2 0.7 48 2 US-08-169-948B-38
C 998 16.2 0.7 48 2 US-08-741-931-2
C 999 16.2 0.7 48 2 US-08-475-228A-19
C1000 16.2 0.7 48 2 US-08-448-873-38

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## ALIGNMENTS

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Sequence 8, Appli
Sequence 210, App
Sequence 210, App
Sequence 8, Appli
Sequence 165, App
Sequence 48, Appl
Sequence 54, Appl
Sequence 839, App
Sequence 840, App
Sequence 1167, Ap
Sequence 1219, Ap
Sequence 1231, Ap
Sequence 165, App
Sequence 35, Appl
Sequence 165, App
Sequence 18, Appl
Sequence 18, Appl
Sequence 2, Appli
Sequence 19, Appl
Sequence 38, Appl
Sequence 19, Appl
Sequence 16, Appl
Sequence 38, Appl

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RESULT 1
US-08-859-998-1322/C
; Sequence 1322, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-1322

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Query Match 1.2%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 859 CTTGAGTCTCAGTGTGATGACCCACAC 886
Db 28 CTTGAGTCTCAGTGTGATGACCCACAC 1

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## RESULT 2

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US-09-225-928-1322/C
; Sequence 1322, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

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Query Match 1.2%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 859 CTTGAGTCTCAGTGTGATGACCCACAC 886
Db 28 CTTGAGTCTCAGTGTGATGACCCACAC 1

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RESULT 3
US-09-382-155-37

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Sequence 37, Application US/09382155B  
Patent No. 6160095  
GENERAL INFORMATION:  
APPLICANT: CHAUDHARY, PREET M  
TITLE OF INVENTION: HOOD, LEROY  
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS  
FILE REFERENCE: Chaudhary  
CURRENT APPLICATION NUMBER: US/09/382,155B  
CURRENT FILING DATE: 1999-08-24  
EARLIER APPLICATION NUMBER: 09/074,044  
EARLIER FILING DATE: 1998-05-07  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 37  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-382-155-37

Query Match 1.2%; Score 27.4; DB 4; Length 29;  
Best Local Similarity 96.6%; Pred. No. 56;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 TCTTCATTACAGCTTGGCCGAGGACCGAG 29

RESULT 4  
US-09-382-155-38/C  
Sequence 38, Application US/09382155B  
Patent No. 6160095  
GENERAL INFORMATION:  
APPLICANT: CHAUDHARY, PREET M  
TITLE OF INVENTION: HOOD, LEROY  
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS  
FILE REFERENCE: Chaudhary  
CURRENT APPLICATION NUMBER: US/09/382,155B  
CURRENT FILING DATE: 1999-08-24  
EARLIER APPLICATION NUMBER: 09/074,044  
EARLIER FILING DATE: 1998-05-07  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 38  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-382-155-38

Query Match 1.2%; Score 27.4; DB 4; Length 29;  
Best Local Similarity 96.6%; Pred. No. 56;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCTTCATTACAGCTTGGCCGAGGACCGAG 613  
|||||  
DB 29 TCTTCATTACAGCTTGGCCGAGGACCGAG 1

RESULT 5  
US-08-859-998-1226/C  
Sequence 1226, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1226:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-1226

Query Match 1.2%; Score 27; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 TCTCACCCTATCCGCTCCATCTTC 1838  
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DB 27 TCTCACCCTATCCGCTCCATCTTC 1

RESULT 6  
US-09-225-928-1226/C  
Sequence 1226, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998

FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1226:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-09-225-928-1226  
SEQUENCE DESCRIPTION: SEQ ID NO: 1226:

Query Match 1.2%; Score 27; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TTCTACCTATCTGCCCTCACATCTTC 1838  
|||||  
Db 27 TTCTACCTATCTGCCCTCACATCTTC 1

RESULT 7  
US-08-859-998-1225  
Sequence 1225, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1225:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA

FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-1225

Query Match 1.1%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1605 TGTACCACACCCAGGCGTATGAGA 1630  
|||||  
Db 1 TTCTACACACCCAGGCGTATGAGA 26

RESULT 8  
US-08-859-998-1321  
Sequence 1321, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1321:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-1321

Query Match 1.1%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 584 TTCTCATTCAGGCTTGCCGAGGAGC 609  
|||||  
Db 1 TTCTCATTCAGGCTTGCCGAGGAGC 26

RESULT 9  
US-09-225-928-1225  
Sequence 1225, Application US/09225928



Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Jokhadze, George  
Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1225:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 1225:  
US-09-225-928-1225  
Query Match 1.1%; Score 26; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1605 TGTACGACACCGAGGCTATGAGGA 1630  
DB 1 TGTACGACACCGAGGCTATGAGGA 26  
RESULT 10  
US-09-225-928-1321  
Sequence 1321, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Jokhadze, George  
Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1321:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 1321:  
US-09-225-928-1321  
Query Match 1.1%; Score 26; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 584 TTCTTCATTGAGGCTTCCGAGGAC 609  
DB 1 TTCTTCATTGAGGCTTCCGAGGAC 26  
RESULT 11  
US-09-171-162B-11  
Sequence 11, Application US/09171162B  
Patent No. 6432701  
GENERAL INFORMATION:  
APPLICANT: Mallet, Jacques  
APPLICANT: Ravassard, Philippe  
APPLICANT: Treilhou, Fabienne  
TITLE OF INVENTION: Derived Tyrosine Hydroxylase Gene Expression System  
FILE REFERENCE: ST96018  
CURRENT APPLICATION NUMBER: US/09/171,162B  
CURRENT FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: PCT/FR97/000636  
PRIOR FILING DATE: 1997-10-04  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 41  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: oligo derived from HUMTHO1  
US-09-171-162B-11  
Query Match 1.0%; Score 22.8; DB 4; Length 41;  
Best Local Similarity 79.4%; Pred. No. 1.6e+03;  
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1978 CTCACAAATTATCATTCATCATTCATTCATT 2011  
DB 3 CTCATCATTCATTCATTCATTCATTCATTCATT 36

```

MATCHES      :    Conserved     U; Mismatches       7; Indels        0; Gaps         0
QY          1978 CTCACCAATTATTCATTTCCATCATCATTGATCTT 2011
           ||||| | | | | | | | | | | | | | | | | | 
Db          16   CTGCATTCATTCATTCATTCATTCATTCATTCATTC 49

RESULT 14
US-09-171-162B-12
// Sequence 12, Application US/0911162B
// Patent No. 6432701
// GENERAL INFORMATION:
// APPLICANT: Mallat, Jacques
// APPLICANT: Meloni, Rolando
// APPLICANT: Ravassard, Philippe
// APPLICANT: Rethelou, Fabienne
// TITLE OF INVENTION: Derived Tyrosine Hydroxylase Gene Expression System
// FILE REFERENCE: ST966018
// CURRENT APPLICATION NUMBER: US/09/171,162B
```

```

RESULT 16
US-09-710-200-59/c
Sequence 59, Application US/09710200
Patent No. 6379897
GENERAL INFORMATION:
APPLICANT: Nanogen, Inc.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Wang, Ling
APPLICANT: Xu, Xiao
APPLICANT: Heller, Michael J.
APPLICANT: Kahl, Brenda F.
TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
FILE REFERENCE: 236/262 Patrick S. Eaglemen
CURRENT APPLICATION NUMBER: US/09/710.200
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 49

```



PRIOR APPLICATION NUMBER: 09/358,972  
PRIOR FILING DATE: 1999-07-21  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TPOX allele  
US-09-383-316-44

Query Match 0.9%; Score 21.2; DB 4; Length 48;  
Best Local Similarity 69.0%; Pred. No. 5.1e+03;  
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1985 ATTATCATCATCATCATTTATTCATTTGGTTCGACATAGT 2026  
DB 45 ATTATCATCATCATCATTTATTCATTTGAGGAGGTTCCCTAGT 4

RESULT 21  
US-08-556-627A-7/C  
Sequence 7, Application US/08556627A  
Patent No. 6462175  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: Mch3, A No. 6462175e1 Apoptotic Protease,  
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,627A  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-556-627A-7

Query Match 0.9%; Score 21; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 AAGTGAAGAGAGATTATGCG 2176  
DB 21 AAGTGAAGAGAGATTATGCG 1

RESULT 22  
US-09-564-805-130/C  
Sequence 130, Application US/09564805  
Patent No. 6333403  
GENERAL INFORMATION:  
APPLICANT: Tavtigian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
CURRENT FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
PRIOR FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 130  
LENGTH: 41  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-564-805-130

Query Match 0.9%; Score 20.8; DB 4; Length 41;  
Best Local Similarity 70.0%; Pred. No. 6.1e+03;  
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1231 CACAGAGAGACTTCTGGAGAAAGCTCATGCTGTCTC 1270  
DB 41 CTACAGACACACTTTTGAAGATGGTCATAGCTGTTCC 2

RESULT 23  
US-08-400-864-1/C  
Sequence 1, Application US/08400864  
Patent No. 5721137  
GENERAL INFORMATION:  
APPLICANT: FRASCOTTI, GIANNI  
APPLICANT: GRANDI, GUIDO  
TITLE OF INVENTION: PLASMID VECTOR AND ITS USE FOR THE  
TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,864  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT 000727 MI94A  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 2264-083-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220

```
TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 49 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-400-864-1

Query Match
Best Local Similarity 0.9%; Score 20.8; DB 1; Length 49;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AACCTGTAGCTTAAATATATATGACACTTTTACATTTCCA 2115
DB 49 AACCTATTTACATTAATAAATTTCTCCTGAAGCAATAAATTTTCTA 2

RESULT 24
US-09-030-156-21/C
; Sequence 21, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human /
; OTHER INFORMATION: Biotin
US-09-030-156-21

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 4; Length 41;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATCATTCATCATCTTATTCATGGGTGTC 2019
DB 40 ATTATTCATTCATTCATTCATTCATGAGGCTTC 6

RESULT 25
US-09-645-757-21/C
; Sequence 21, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human /
; OTHER INFORMATION: Biotin
US-09-645-757-21

Query Match
0.9%; Score 20.6; DB 4; Length 41;
Score 20.6; DB 4; Length 41;
```

```
Best Local Similarity 74.3%; Pred. No. 7e+03;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATCATTCATCATCTTATTCATGGGTGTC 2019
DB 40 ATTATTCATTCATTCATTCATTCATGAGGCTTC 6

RESULT 26
US-09-030-156-5
; Sequence 5, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-09-030-156-5

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 4; Length 45;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATCATTCATCATCTTATTCAT 2011
DB 19 ATTATTCATTCATTCATTCATTCAT 45

RESULT 27
US-09-645-757-5
; Sequence 5, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-09-645-757-5

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 4; Length 45;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATCATTCATCATCTTATTCAT 2011
DB 19 ATTATTCATTCATTCATTCATTCAT 45

RESULT 28
US-09-641-638-1284
; Sequence 1284, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
```

APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENEST.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 1284  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 10-350-72 : polymorphic base C or T  
US-09-641-638-1284

Query Match 0.9%; Score 20.2; DB 4; Length 47;  
Best Local Similarity 75.8%; Pred. No. 1e+04;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1670 ATCATCCAGAGAGAGCTGGAACCATGATGGGAGC 1702  
|||||  
Db 6 AGCATCAAGAGAGAGAGCTGATGCTGGGATGC 38

RESULT 29  
US-07-828-444-7  
Sequence 7, Application US/07828444  
Patent No. 5290677  
GENERAL INFORMATION:  
APPLICANT: ROBERTSON, BETTY H.  
APPLICANT: NAIMAN, OMANA V.  
APPLICANT: BROWN, VICKI K.  
APPLICANT: MARGOLIS, HAROLD S.  
APPLICANT: KHANNA, BHAWNA  
TITLE OF INVENTION: RAPID AND SENSITIVE TEST FOR DETECTING  
TITLE OF INVENTION: HEPATITIS A VIRUS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/828,444  
FILING DATE: 19920131  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SCOTT, WATSON T.  
REGISTRATION NUMBER: 26,581  
REFERENCE/DOCKET NUMBER: 5683/91979  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3067

TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-828-444-7

Query Match 0.9%; Score 20.2; DB 1; Length 50;  
Best Local Similarity 75.8%; Pred. No. 1e+04;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 501 AAGATGTCACACCAATTAAGATTGACAG 533  
|||||  
Db 15 AAGTTGTATCACACACTGAAGATCTTAAG 47

RESULT 30  
US-08-863-639A-25/c  
Sequence 25, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Muelth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-25

Query Match 0.9%; Score 20; DB 2; Length 36;  
Best Local Similarity 72.2%; Pred. No. 9.6e+03;  
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1892 GGAAGAGCAAGGAGACAGTGAAGCAGGAAGAAGAA 1927  
|||||  
Db 36 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1

RESULT 31

US-08-938-830-31  
; Sequence 31, Application US/08938830  
; Patent No. 6040437  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Laurence A.  
; APPLICANT: Dowbenko, Donald J.  
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
; TITLE OF INVENTION: Furrow-Associated Proteins (FSTRIPS)  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,830  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/798419  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1066P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-3216  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-08-938-830-31  
Query Match 0.9%; Score 20; DB 3; Length 42;  
Best Local Similarity 72.2%; Pred. No. 1.1e+04;  
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 777 TCTGCTCATCTGGAGGACGAGAAAGACCTGG 812  
|| ||||| ||||| ||||| ||||| |||||  
Db 5 TCGATCCATGATGAGAGAGGTACGGAAGAGCTGG 40  
RESULT 32  
US-09-641-638-1118  
; Sequence 1118, Application US/09641638  
; Patent No. 6432648  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
; FILE REFERENCE: GENSET 051CPI  
; CURRENT APPLICATION NUMBER: US/09/641,638  
; CURRENT FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/275,267  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: US 60/119,917

PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 1304  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1118  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 10-276-407 : polymorphic base C or T  
US-09-641-638-1118  
Query Match 0.9%; Score 20; DB 4; Length 47;  
Best Local Similarity 76.7%; Pred. No. 1.1e+04;  
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1170 TTCCTTAAGATTATTTCTCTTGTATG 1199  
|| ||| ||||| ||||| ||||| |||||  
Db 2 TTACCTTATATATATTTCTCTCAGATATG 31  
RESULT 33  
US-08-316-439A-31/C  
; Sequence 31, Application US/08316439A  
; Patent No. 5840520  
; GENERAL INFORMATION:  
; APPLICANT: CLARKE, DAVID KIRKWOOD  
; APPLICANT: PABESE, PETER M  
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION  
; TITLE OF INVENTION: SYSTEMS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM  
; STREET: FIVE PALO ALTO SQUARE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,439A  
; FILING DATE: September 30, 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/190,678  
; FILING DATE: February 1, 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,061  
; FILING DATE: August 4, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/527,237  
; FILING DATE: May 22, 1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/399,728  
; FILING DATE: August 28, 1989  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CSERR, UDANN  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: AVIR-010/00US  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 843-5165  
TELEFAX: (415) 857-0663  
TELEX: 380816 COOLY PA  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: SYNTHETIC DNA  
US-08-316-439A-31

Query Match 0.9%; Score 20; DB 2; Length 50;  
Best Local Similarity 65.9%; Pred. No. 1.2e+04;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2083 TAAATATATCTGGAACCTTTAGATTTCCAGCCTTATTT 2126  
DB 48 TTAATTTAAGTGCTATCATCAATCTTATTTGCCCATTTT 5

RESULT 34  
US-09-276-533A-6/c  
Sequence 6, Application US/09276533A  
Patent No. 6436707

GENERAL INFORMATION:  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Friedrich, Glenn A.  
APPLICANT: Lilleberg, Stan  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: VECTORS FOR GENE MUTAGENESIS AND GENE  
FILE REFERENCE: 07705-0006-00000  
CURRENT FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: US/09/276,533A  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/079,729  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/109,302  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 43  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-276-533A-6

Query Match 0.9%; Score 19.8; DB 4; Length 43;  
Best Local Similarity 69.2%; Pred. No. 1.2e+04;  
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 727 CTATTACTCGTGAGAGCCGAGAGAGGCTCGTGT 765  
DB 41 CTGTTGTCATGAGAGGAAGGCGACAGTACTGCTT 3

RESULT 35  
US-09-158-863C-32/c  
Sequence 32, Application US/09158863C  
Patent No. 6280978  
GENERAL INFORMATION:  
APPLICANT: Mitchell, Lloyd G.  
APPLICANT: Garcia-Blanco, Mariano A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN  
FILE REFERENCE: 31304-B-A  
CURRENT APPLICATION NUMBER: US/09/158,863C  
CURRENT FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 09/133,717  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: 09/087,233

PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 08/766,354  
PRIOR FILING DATE: 1996-12-13  
PRIOR APPLICATION NUMBER: 60/008,317  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer complementary to the  
US-09-158-863C-32

Query Match 0.9%; Score 19.8; DB 4; Length 47;  
Best Local Similarity 63.8%; Pred. No. 1.3e+04;  
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 880 CCCACACTTCATGAGAGAGACAGTCCCTGTGTCTCCATGC 926  
DB 47 CACCCAGTCCCATTTATGAGCAGAGCCGCTGAGGGTTACCATGC 1

RESULT 36  
US-09-171-162B-13  
Sequence 13, Application US/09171162B  
Patent No. 6432701  
GENERAL INFORMATION:  
APPLICANT: Mallet, Jacques  
APPLICANT: Meloni, Rolando  
APPLICANT: Ravassard, Philippe  
APPLICANT: Treillhou, Fabienne  
TITLE OF INVENTION: Derived Tyrosine Hydroxylase Gene Expression System  
FILE REFERENCE: ST96018  
CURRENT APPLICATION NUMBER: US/09/171,162B  
CURRENT FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: PCT/FR97/00636  
PRIOR FILING DATE: 1997-10-04  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: oligo derived from HUWTH01  
US-09-171-162B-13

Query Match 0.8%; Score 19.6; DB 4; Length 31;  
Best Local Similarity 84.6%; Pred. No. 1.1e+04;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATGCAATCAATCAATTTATTCAT 2010  
DB 6 ATTCATTCATTCATTCATTCATTCAT 31

RESULT 37  
PCT-US96-03916-35  
Sequence 35, Application PC/TUS9603916  
GENERAL INFORMATION:  
APPLICANT: Wild, Martha A.  
APPLICANT: Cochran, Mark D.  
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York



COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03916  
FILING DATE: 23-MAR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,597  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 39116-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US96-03916-35

Query Match 0.8%; Score 19.6; DB 5; Length 42;  
Best Local Similarity 73.5%; Pred. No. 1.4e+04;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1667 GGCATCATCCAGAGAGCTGGACCATGCTGGGG 1700  
||||| 11111 111111111 1  
Db 6 GGATCCTCTAGAGTCGAGGACCATGCTGGCG 39

RESULT 38  
US-08-801-898A-27  
Sequence 27, Application US/08801898A  
Patent No. 5998602  
GENERAL INFORMATION:  
APPLICANT: Torrence, Paul F.  
APPLICANT: Silverman, Robert H.  
APPLICANT: Cirino, Nick M.  
APPLICANT: Li, Guyling  
APPLICANT: Xiao, Wei  
TITLE OF INVENTION: RAS-1 ACTIVATORS AND ANTISENSE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,898A  
FILING DATE: 18-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Polsant, Brian M.  
REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8656-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: Oligonucleotide  
LOCATION: 1...49  
OTHER INFORMATION: SPA4-antIRSV3'-3'/(8251-8299)  
US-08-801-898A-27

Query Match 0.8%; Score 19.6; DB 2; Length 49;  
Best Local Similarity 66.7%; Pred. No. 1.5e+04;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2181 ATTTGGCATTGTTGTTTCAGATGCTTATCTTTGAAT 2222  
||||| 11111 111111111 111111111 1  
Db 7 ATTTGGTTGTTTGTATGAAATATAGTGTTCTTTGATT 48

RESULT 39  
US-08-556-627A-9/C  
Sequence 9, Application US/08556627A  
Patent No. 6462175  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomasetti, Kevin  
TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,  
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,627A  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-556-627A-9

Query Match 0.8%; Score 19.4; DB 4; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1e+04;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 GATGCATCCAGCCGACGCG 640

Db 21 GATGCATCCAGCCGACTAG 1

RESULT 40

US-08-231-342-17/c

Sequence 17, Application US/08231342

Patent No. 5827684

GENERAL INFORMATION:

APPLICANT: Sreekrishna, Kotikanyadanam

APPLICANT: Prevatt, William D

APPLICANT: Thill, Gregory P

APPLICANT: Davis, Geneva R

APPLICANT: Koutz, Patricia

APPLICANT: Barr, Kathryn A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

APPLICANT: Hopkins, Sharon A

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

FILE REFERENCE: GENSET.031A

CURRENT APPLICATION NUMBER: US/09/345,882

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: US 60/091,315

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/111,909

PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patent.pm

SEQ ID NO 71

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 1..47

OTHER INFORMATION: polymorphic fragment 99-1442-224, variant version of SEQ ID50

NAME/KEY: allele

LOCATION: 24

OTHER INFORMATION: base T ; G in SEQ ID50

FEATURE:

NAME/KEY: primer\_bind

LOCATION: 1..23

OTHER INFORMATION: potential microsequencing oligo 99-1442-224.mis1

NAME/KEY: primer\_bind

LOCATION: 25..47

OTHER INFORMATION: complement potential microsequencing oligo 99-1442-224.mis2

US-09-345-882-71

Query Match

Best Local Similarity 0.8%; Score 19.4; DB 4; Length 47;

Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2107 ATTATCCAGCCTATTGAGTAATAATTGTTACTTTAGT 2151

Db 1 ATTATCCAGCCTATTGAGTATTTGTTCTCTCTTAAT 45

RESULT 42

US-08-843-409-11/c

Sequence 11, Application US/08843409

Patent No. 6103235

GENERAL INFORMATION:

APPLICANT: Neville, David M.

APPLICANT: Scharif, Joshua E.

APPLICANT: Thompson, Jerry Todd

APPLICANT: Hu, Hualzhong

APPLICANT: Ma, Shenglin

TITLE OF INVENTION: AN IMMUNOTOXIN WITH IN VIVO T CELL

FILE REFERENCE: 14014.0205

CURRENT APPLICATION NUMBER: US/08/843,409

CURRENT FILING DATE: 1997-04-15

EARLIER APPLICATION NUMBER: 08/739,703

EARLIER FILING DATE: 1996-10-29

EARLIER APPLICATION NUMBER: 60/008,104

EARLIER FILING DATE: 1995-10-30

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 11

LENGTH: 36

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide primer

OTHER INFORMATION: y is c or t

US-08-843-409-11

Query Match

Best Local Similarity 0.8%; Score 19.2; DB 3; Length 36;

Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2107 ATTATCCAGCCTATTGAGTAATAATTGTTACTTTAGT 2151

Db 1 ATTATCCAGCCTATTGAGTATTTGTTCTCTCTTAAT 45

	Matches	24;	Conservative	1;	Mismatches	9;	Indels	0;	Gaps	0;
QY	1865	TCGTGAGCCACCTCAGCAAGGACCTTGGAGAG	1898							
Db	36	TTTGGGAGGACGCTCGCAATTAAGCTTTCAGAG	3							

RESULT 43  
US-08-484

```

: Sequence 17, Application US/08484397A
: Patent No. 5869055
:
: GENERAL INFORMATION:
: APPLICANT: Juan, Shao-Chieh
: APPLICANT: Lichenstein, Henri S.
: APPLICANT: Wright, Samuel D.
: TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: AMGEN INC
: STREET: 1840 Dehavilland Drive
: CITY: Thousand Oaks
: STATE: CA
: COUNTRY: US
: ZIP: 91320-1789
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,397A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Curry, Daniel R.
: REGISTRATION NUMBER: 32,727
: REFERENCE/DOCKET NUMBER: A-324A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 805/447-1000
: TELEFAX: 805/447-1090
: INFORMATION FOR SEQ. ID NO: 17:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 41 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: CDNA
:
: US-08-484-397A-17

```

Query Match	0.88	Score 19.2	DB 2	Length 41
Best Local Similarity	67.58	Pred. No. 1.8e+04		
Matches 27	Conservative	13	Indels	0
			Gaps	0

RESULT 44  
US-09-546-483-2/C  
; Sequence 2, Application US/09546483  
; Patent No. 6358739  
; GENERAL INFORMATION:  
; APPLICANT: Baetge, Ed  
; APPLICANT: Wong, Shou  
; APPLICANT: Duprez, Philippe  
; APPLICANT: Thorens, Bernard  
; TITLE OF INVENTION: "TRANSIENTLY IMMORTALIZED CELLS FOR USE IN GENE THERAPY"  
; FILE REFERENCE: 17811-011  
; CURRENT APPLICATION NUMBER: US/09/546,483  
; CURRENT FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/128,893  
; PRIOR FILING DATE: 1999-04-12

```

? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 2
? LENGTH: 41
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-546-483-2

```

07	184	CATCAAGACACCCGGGAGCCGAGTGCCTCAT	215	
Db	32	CTTCAAGACCATCTCGAGCTGAATTCATATAT	1	

OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER  
US-09-823-177-2

RESULT 46  
 US-08-746-111-40/c  
 : Sequence 40, Application US/08746111  
 : Patent No. 6066778  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Ginsburg, David  
 :  
 : APPLICANT: Gu, Jisong  
 :  
 : TITLE OF INVENTION: Compositions And Methods For Screening  
 : TITLE OF INVENTION: Compounds For Anticoagulant Activity  
 :  
 : NUMBER OF SEQUENCES: 54  
 :  
 : CORRESPONDENCE ADDRESS:  
 :  
 : ADDRESSEE: Medlen & Carroll, LLP  
 : STREET: 220 Montgomery Street, Suite 2200  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States of America  
 :  
 : ZIP: 94104  
 :  
 : COMPUTER READABLE FORM:  
 :

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/746,111  
FILING DATE: 06-NOV-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
TELEPHONE/DOCKET NUMBER: UM-02536  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-746-111-40

Query Match 0.8%; Score 19.2; DB 3; Length 42;  
Best Local Similarity 67.5%; Pred. No. 1.8e+04;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY \* 1446 TCATATGACTTGAGAGAGAAAGCTTATGATTCGATA 1485  
DB 40 TCATAGAGACAGAGAGAGAAAGCTGAAAGCTCAGAGAA 1

RESULT 47  
US-09-284-832-29  
Sequence 29; Application US/09284832  
Patent No. 6287770  
GENERAL INFORMATION:  
APPLICANT: WESTON, Anthony  
APPLICANT: ASSENBERG, Rene  
APPLICANT: MARSH, Peter  
APPLICANT: MOCK, Graham Andrew  
APPLICANT: RAY, Trevor Duncan  
APPLICANT: WHARAM, Susan Deborah  
APPLICANT: CARLY, Donald Leonard Nicholas  
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO NUCLEIC ACID PROMOTERS  
FILE REFERENCE: 41301/2258923  
CURRENT APPLICATION NUMBER: US/09/284,832  
EARLIER FILING DATE: 1998-04-16  
EARLIER FILING NUMBER: GB 9801627.2  
EARLIER FILING DATE: 1998-01-27  
EARLIER APPLICATION NUMBER: GB 9814697.0  
EARLIER FILING DATE: 1998-07-08  
EARLIER APPLICATION NUMBER: PCT/GB99/00265  
EARLIER FILING DATE: 1999-01-26  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 29  
LENGTH: 45  
TYPE: DNA  
ORGANISM: CFTR CS Probe with SP6 Promoter  
US-09-284-832-29

Query Match 0.8%; Score 19.2; DB 4; Length 45;  
Best Local Similarity 67.5%; Pred. No. 1.9e+04;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 250 ATGCATCATATATAACAGCAAGACTTGATTAAGTGACA 289  
DB 1 ATTTCATCATAGGAACACCAAGATGATATTAGGTGACA 40

RESULT 48

US-09-641-638-931/c  
Sequence 931; Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bouguetel, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
FILE REFERENCE: GENSET.051Cp1  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent. pm  
SEQ ID NO 931  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 12-834-183 : polymorphic base A or G  
US-09-641-638-931

Query Match 0.8%; Score 19.2; DB 4; Length 47;  
Best Local Similarity 70.6%; Pred. No. 2e+04;  
Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1134 TTTTATATGTTTATTCATTTGTCAGCTGTGTA 1167  
DB 35 TTTGTTTACAYTGTTTCATTTGTCAGCTGAGAA 2

RESULT 49  
US-08-471-791-35/c  
Sequence 35; Application US/08471791  
Patent No. 5723595  
GENERAL INFORMATION:  
APPLICANT: Thompson, Gregory A  
APPLICANT: Knaut, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1 (a)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,791  
FILING DATE: 6-JUNE-95  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/762,762  
FILING DATE: 16-SEPT-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/01746  
FILING DATE: 14-MAR-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/615,784  
FILING DATE: 14-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/567,373  
FILING DATE: 13-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/494,106  
FILING DATE: 16-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lassen, Elizabeth  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE 69-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
TELEX: 350370 CGNE  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: synthetic oligonucleotide  
US-08-471-791-35

Query Match 0.8%; Score 19.2; DB 1; Length 48;  
Best Local Similarity 67.5%; Pred. No. 2e+04;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 155 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194  
Db 47 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 8

RESULT 50  
PCT-US91-01746-35/C  
Sequence 35, Application PC/TUS9101746  
GENERAL INFORMATION:  
APPLICANT: Thompson, Gregory A  
APPLICANT: Knaut, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/01746  
FILING DATE: 19910314  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/615,784  
FILING DATE: 14-NOV-1990  
APPLICATION NUMBER: 07/567,373  
FILING DATE: 13-AUG-1990  
APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lassen, Elizabeth  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
TELEX: 350370 CGNE  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: synthetic oligonucleotide  
PCT-US91-01746-35

Query Match 0.8%; Score 19.2; DB 5; Length 48;  
Best Local Similarity 67.5%; Pred. No. 2e+04;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 155 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194  
Db 47 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 8

Search completed: November 11, 2002, 02:36:25  
Job time: 117 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 00:01:12 ; Search time 131 Seconds  
(without alignments)  
6253.432 Million cell updates/sec

Title: US-09-659-860A-3  
Perfect score: 2309  
Sequence: 1 gagagacgtgcacatccca.....gattaaatgtgtgtt 2309

Scoring table:  
IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 17792727 residues

Total number of hits satisfying chosen parameters: 164392

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications -NA: \*  
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2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq: \*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq: \*  
4: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq: \*  
5: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq: \*  
6: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq: \*  
7: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq: \*  
8: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq: \*  
9: /cgn2\_6/prodata/1/pubpna/US05\_PUBCOMB.seq: \*  
10: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq: \*  
11: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*  
12: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq: \*  
13: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq: \*  
14: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.8	1.0	49	12	US-10-108-280-6
2	21.8	0.9	49	10	US-09-975-408-59
3	21.8	0.9	49	12	US-10-075-579-59
4	21.4	0.9	45	10	US-09-820-171-27
5	21.2	0.9	48	10	US-09-790-417-150
6	21.0	0.9	21	10	US-09-944-851-7
7	20.6	0.9	41	12	US-10-108-280-21
8	20.6	0.9	45	12	US-09-839-743-28
9	20.6	0.9	44	10	US-09-756-095-32
10	19.8	0.9	47	10	US-09-944-851-9
11	19.4	0.8	43	10	US-09-774-021-17
12	19.4	0.8	40	10	US-09-809-905-4
13	19.2	0.8	19	10	US-09-944-851-5
14	19.0	0.8	46	9	US-09-884-260A-48
15	19.0	0.8	35	9	US-09-284-249-2
16	18.6	0.8	39	10	US-09-867-262-13
17	18.6	0.8	39	10	US-09-885-551A-13
18	18.6	0.8	39	12	US-10-087-426-13
19	18.6	0.8	39	12	US-10-087-426-13

20	18.6	0.8	41	12	US-10-108-280-4	Sequence 4, Appl1
21	18.6	0.8	42	10	US-09-997-956-3	Sequence 1, Appl1
22	18.4	0.8	46	9	US-09-771-372-1	Sequence 14, Appl1
23	18.4	0.8	50	9	US-09-440-829-14	Sequence 5, Appl1
24	18.2	0.8	50	10	US-09-734-836-5	Sequence 8, Appl1
25	18.0	0.8	18	10	US-09-944-851-11	Sequence 11, Appl1
26	18.0	0.8	18	10	US-09-944-851-11	Sequence 10, Appl1
27	18.0	0.8	21	10	US-09-944-851-11	Sequence 743, Appl1
28	18.0	0.8	37	10	US-09-263-959-743	Sequence 801, Appl1
29	18.0	0.8	37	10	US-09-784-990-33	Sequence 33, Appl1
30	17.8	0.8	31	10	US-09-839-743-1	Sequence 1, Appl1
31	17.8	0.8	36	10	US-10-081-281-11	Sequence 11, Appl1
32	17.8	0.8	37	12	US-09-962-055-30	Sequence 30, Appl1
33	17.8	0.8	45	10	US-10-023-529-30	Sequence 30, Appl1
34	17.8	0.8	45	12	US-10-023-523-30	Sequence 30, Appl1
35	17.8	0.8	48	9	US-09-956-086-32	Sequence 32, Appl1
36	17.8	0.8	48	9	US-09-956-087-32	Sequence 32, Appl1
37	17.8	0.8	50	9	US-09-440-829-26	Sequence 26, Appl1
38	17.8	0.8	50	9	US-09-334-923A-49	Sequence 49, Appl1
39	17.6	0.8	28	10	US-09-334-954A-49	Sequence 13, Appl1
40	17.6	0.8	36	9	US-09-985-442-13	Sequence 40, Appl1
41	17.6	0.8	36	10	US-09-935-727-40	Sequence 13, Appl1
42	17.6	0.8	36	10	US-09-983-580-13	Sequence 18, Appl1
43	17.6	0.8	40	10	US-09-834-291-18	Sequence 26, Appl1
44	17.6	0.8	40	10	US-09-834-291-18	Sequence 29, Appl1
45	17.6	0.8	41	10	US-09-238-351-29	Sequence 3, Appl1
46	17.6	0.8	42	10	US-09-737-626A-3	Sequence 18, Appl1
47	17.6	0.8	45	9	US-10-104-611-18	Sequence 18, Appl1
48	17.6	0.8	45	9	US-10-112-547-18	Sequence 32, Appl1
49	17.6	0.8	45	10	US-09-965-602-27	Sequence 27, Appl1
50	17.6	0.8	45	10	US-09-872-349-32	Sequence 44, Appl1
51	17.6	0.8	48	10	US-09-056-160B-44	Sequence 59, Appl1
52	17.6	0.8	49	9	US-09-858-200A-1	Sequence 14, Appl1
53	17.6	0.8	39	9	US-09-252-150-59	Sequence 14, Appl1
54	17.4	0.8	42	10	US-09-749-234A-14	Sequence 56, Appl1
55	17.4	0.8	44	10	US-09-988-899-56	Sequence 24, Appl1
56	17.4	0.8	44	10	US-09-900-062-24	Sequence 51, Appl1
57	17.4	0.8	47	9	US-09-935-371-51	Sequence 98, Appl1
58	17.4	0.8	47	10	US-09-374-671-98	Sequence 163, Appl1
59	17.4	0.8	50	9	US-09-992-598-163	Sequence 163, Appl1
60	17.4	0.8	50	10	US-09-504-221A-3057	Sequence 269, Appl1
61	17.4	0.8	50	10	US-09-810-936-269	Sequence 163, Appl1
62	17.4	0.8	50	10	US-09-989-722-163	Sequence 163, Appl1
63	17.4	0.8	50	10	US-09-989-723-163	Sequence 163, Appl1
64	17.4	0.8	50	10	US-09-989-723-163	Sequence 163, Appl1
65	17.4	0.8	50	10	US-09-989-279-163	Sequence 163, Appl1
66	17.4	0.8	50	10	US-09-989-727-163	Sequence 163, Appl1
67	17.4	0.8	50	10	US-09-274-553D-3057	Sequence 163, Appl1
68	17.4	0.8	50	10	US-09-989-731-163	Sequence 163, Appl1
69	17.4	0.8	50	10	US-09-429-755-269	Sequence 269, Appl1
70	17.4	0.8	50	10	US-09-989-732-163	Sequence 163, Appl1
71	17.4	0.8	50	10	US-09-991-073-163	Sequence 163, Appl1
72	17.4	0.8	50	10	US-09-990-442-163	Sequence 163, Appl1
73	17.4	0.8	50	10	US-09-991-163-163	Sequence 163, Appl1
74	17.4	0.8	50	10	US-09-993-604-163	Sequence 163, Appl1
75	17.4	0.8	50	10	US-09-990-456-163	Sequence 163, Appl1
76	17.4	0.8	50	10	US-09-989-721-163	Sequence 163, Appl1
77	17.4	0.8	50	10	US-09-297-910-13	Sequence 14, Appl1
78	17.4	0.8	50	10	US-09-327-910-14	Sequence 81, Appl1
79	17.2	0.7	30	10	US-09-971-187-6	Sequence 6, Appl1
80	17.2	0.7	34	10	US-09-952-385-4	Sequence 4, Appl1
81	17.2	0.7	35	12	US-10-000-759A-4	Sequence 1, Appl1
82	17.2	0.7	37	10	US-09-758-317-1	Sequence 25, Appl1
83	17.2	0.7	40	9	US-09-863-040-25	Sequence 25, Appl1
84	17.2	0.7	40	9	US-09-238-351-73	Sequence 73, Appl1
85	17.2	0.7	40	10	US-09-238-351-40	Sequence 40, Appl1
86	17.2	0.7	41	10	US-09-803-165-2	Sequence 3036, Appl1
87	17.2	0.7	44	10	US-09-504-231A-3036	Sequence 3036, Appl1
88	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Appl1
89	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Appl1
90	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Appl1
91	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Appl1
92	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Appl1

93	17	0.7	20	10	US-09-825-922-5	Sequence 5, Appli	166	16.2	0.7	30	9	US-09-982-107-15	Sequence 16, Appli
C 94	17	0.7	30	9	US-09-840-243B-8	Sequence 8, Appli	C 167	16.2	0.7	30	10	US-09-760-574-99	Sequence 99, Appli
95	17	0.7	30	10	US-09-272-162-7	Sequence 7, Appli	C 168	16.2	0.7	30	10	US-09-765-272-417	Sequence 417, Appl
96	17	0.7	35	8	US-09-973-028-9	Sequence 9, Appli	169	16.2	0.7	30	10	US-09-333-527-18	Sequence 18, Appl
97	17	0.7	36	9	US-09-985-442-12	Sequence 12, Appli	170	16.2	0.7	31	10	US-09-801-274-84	Sequence 81, Appli
98	17	0.7	36	9	US-09-848-164-114	Sequence 114, Appl	C 171	16.2	0.7	31	10	US-09-801-274-84	Sequence 94, Appli
99	17	0.7	36	10	US-09-983-580-12	Sequence 12, Appli	172	16.2	0.7	31	10	US-09-263-059-880	Sequence 560, Appl
100	17	0.7	43	10	US-09-993-170-21	Sequence 21, Appli	173	16.2	0.7	32	10	US-09-982-308-20	Sequence 20, Appli
C 101	17	0.7	44	10	US-09-993-170-21	Sequence 21, Appli	174	16.2	0.7	38	10	US-09-784-990-24	Sequence 24, Appli
C 102	17	0.7	45	10	US-09-803-165-4	Sequence 4, Appli	175	16.2	0.7	38	10	US-09-874-547-84	Sequence 84, Appli
103	17	0.7	45	10	US-09-765-873A-3	Sequence 3, Appli	176	16.2	0.7	40	9	US-10-007-448-4	Sequence 4, Appli
104	17	0.7	45	10	US-09-918-889-28	Sequence 28, Appli	C 177	16.2	0.7	40	9	US-09-863-040-25	Sequence 25, Appli
105	17	0.7	45	10	US-09-919-042-23	Sequence 23, Appli	C 178	16.2	0.7	40	9	US-09-863-040-25	Sequence 26, Appli
C 106	17	0.7	45	10	US-09-765-272-235	Sequence 235, Appl	179	16.2	0.7	40	10	US-09-728-847-31	Sequence 31, Appli
C 107	17	0.7	50	10	US-09-504-231A-2961	Sequence 2961, Ap	C 180	16.2	0.7	40	10	US-09-027-287-11	Sequence 11, Appli
C 108	17	0.7	50	10	US-09-274-553D-3048	Sequence 3048, Ap	C 181	16.2	0.7	40	10	US-09-027-287-11	Sequence 15, Appli
C 109	16.8	0.7	31	10	US-09-801-274-72	Sequence 28, Appl	C 182	16.2	0.7	40	10	US-09-252-656B-11	Sequence 11, Appli
110	16.8	0.7	33	10	US-09-976-118-10	Sequence 10, Appli	C 183	16.2	0.7	43	9	US-09-252-656B-15	Sequence 15, Appli
111	16.8	0.7	33	10	US-09-971-253-10	Sequence 10, Appli	C 184	16.2	0.7	44	10	US-10-081-408-7	Sequence 7, Appli
112	16.8	0.7	33	10	US-09-911-611-21	Sequence 21, Appli	C 185	16.2	0.7	44	10	US-09-803-165-3	Sequence 3, Appli
113	16.8	0.7	37	12	US-09-883-489-4	Sequence 4, Appli	C 186	16.2	0.7	44	10	US-09-803-165-5	Sequence 5, Appli
114	16.8	0.7	36	10	US-09-883-489-4	Sequence 4, Appli	C 187	16.2	0.7	44	10	US-09-803-165-7	Sequence 7, Appli
C 115	16.8	0.7	39	10	US-09-774-414-30	Sequence 30, Appli	C 188	16.2	0.7	44	10	US-09-803-165-7	Sequence 19, Appli
C 116	16.8	0.7	41	10	US-09-782-361-18	Sequence 18, Appli	189	16.2	0.7	46	10	US-09-835-147-22	Sequence 22, Appli
C 117	16.8	0.7	42	9	US-09-996-140-29	Sequence 29, Appli	C 190	16.2	0.7	47	10	US-09-816-825-8	Sequence 8, Appli
C 118	16.8	0.7	42	10	US-09-764-304-13	Sequence 13, Appli	C 191	16.2	0.7	47	10	US-09-908-599-20	Sequence 20, Appli
119	16.8	0.7	48	10	US-09-756-551A-14	Sequence 14, Appli	C 192	16.2	0.7	47	10	US-09-908-599-20	Sequence 22, Appli
C 120	16.8	0.7	50	9	US-09-440-829-32	Sequence 32, Appli	C 193	16.2	0.7	47	10	US-09-908-599-20	Sequence 22, Appli
C 121	16.6	0.7	34	10	US-09-932-678-6	Sequence 6, Appli	C 194	16.2	0.7	47	10	US-09-901-484A-210	Sequence 210, Appl
C 122	16.6	0.7	36	10	US-09-839-743-1	Sequence 1, Appli	195	16.2	0.7	48	10	US-09-978-273-7	Sequence 7, Appli
C 123	16.6	0.7	40	10	US-09-951-401-25	Sequence 25, Appli	196	16.2	0.7	48	10	US-09-855-797A-56	Sequence 56, Appli
124	16.6	0.7	40	10	US-09-922-101-25	Sequence 25, Appli	197	16.2	0.7	50	9	US-09-931-087A-33	Sequence 33, Appli
C 125	16.6	0.7	42	10	US-09-755-633-2	Sequence 32, Appli	C 198	16.2	0.7	50	10	US-09-909-496-2	Sequence 6, Appli
C 126	16.6	0.7	46	9	US-09-905-291A-32	Sequence 32, Appli	C 199	16.2	0.7	50	10	US-09-909-496-2	Sequence 2, Appli
C 127	16.6	0.7	46	10	US-09-909-920-32	Sequence 32, Appli	C 200	16.2	0.7	50	10	US-09-911-047-2	Sequence 2, Appli
C 128	16.6	0.7	46	10	US-09-909-920-32	Sequence 32, Appli	C 201	16.2	0.7	50	10	US-09-911-047-3	Sequence 3, Appli
C 129	16.6	0.7	47	10	US-09-901-684A-324	Sequence 324, App	C 202	16.2	0.7	50	12	US-10-120-092-2	Sequence 2, Appli
C 130	16.6	0.7	50	9	US-09-978-295A-167	Sequence 167, App	C 203	16.2	0.7	50	12	US-10-120-092-3	Sequence 3, Appli
C 131	16.4	0.7	20	10	US-09-263-959-459	Sequence 459, App	C 204	16	0.7	25	10	US-09-866-108-13693	Sequence 13693, A
C 132	16.4	0.7	31	10	US-09-907-574-1	Sequence 1, Appli	C 205	16	0.7	25	10	US-09-866-108-13694	Sequence 13694, A
C 133	16.4	0.7	31	10	US-09-068-528B-1	Sequence 1, Appli	C 206	16	0.7	25	10	US-09-866-108-13406	Sequence 15406, A
134	16.4	0.7	33	9	US-09-729-520-8	Sequence 8, Appli	C 207	16	0.7	25	10	US-09-866-108-15407	Sequence 15407, A
135	16.4	0.7	33	9	US-10-008-620-8	Sequence 8, Appli	C 208	16	0.7	31	10	US-09-801-274-558	Sequence 558, App
C 136	16.4	0.7	35	10	US-09-940-037A-26	Sequence 26, Appli	C 209	16	0.7	31	10	US-09-801-274-557	Sequence 567, App
C 137	16.4	0.7	36	10	US-09-895-211-9	Sequence 9, Appli	C 210	16	0.7	31	10	US-09-801-274-557	Sequence 823, App
C 138	16.4	0.7	36	12	US-10-127-733-5	Sequence 5, Appli	C 211	16	0.7	31	10	US-09-801-274-557	Sequence 823, App
C 139	16.4	0.7	38	8	US-08-424-550B-623	Sequence 623, App	C 212	16	0.7	33	10	US-09-822-261-102	Sequence 102, App
C 140	16.4	0.7	39	10	US-09-903-456-112	Sequence 112, App	C 213	16	0.7	34	9	US-09-771-009-67	Sequence 67, Appli
C 141	16.4	0.7	40	10	US-09-264-468B-12	Sequence 12, Appli	C 214	16	0.7	35	10	US-09-426-548-34	Sequence 34, Appli
142	16.4	0.7	41	10	US-09-371-307-37	Sequence 37, Appli	C 215	16	0.7	35	10	US-09-732-561-12	Sequence 92, Appli
143	16.4	0.7	45	9	US-09-980-046-21	Sequence 21, Appli	C 216	16	0.7	36	10	US-09-848-164-92	Sequence 92, Appli
144	16.4	0.7	45	10	US-09-827-289-14	Sequence 14, Appli	C 217	16	0.7	37	10	US-09-765-272-340	Sequence 340, Appl
145	16.4	0.7	45	10	US-09-827-289-14	Sequence 14, Appli	C 218	16	0.7	38	10	US-09-774-414-31	Sequence 31, Appli
C 146	16.4	0.7	45	10	US-09-777-430A-24	Sequence 24, Appli	C 219	16	0.7	39	10	US-09-865-579A-27	Sequence 27, Appli
C 147	16.4	0.7	45	10	US-09-795-006A-38	Sequence 38, Appli	C 220	16	0.7	39	10	US-09-921-942B-3	Sequence 3, Appli
C 148	16.4	0.7	46	10	US-09-795-006A-29	Sequence 29, Appli	C 221	16	0.7	40	10	US-09-738-847-27	Sequence 27, Appli
149	16.4	0.7	47	10	US-09-853-798-1	Sequence 1, Appli	C 222	16	0.7	40	10	US-09-955-909-9	Sequence 9, Appli
150	16.4	0.7	48	10	US-09-916-940-66	Sequence 66, Appli	C 223	16	0.7	40	10	US-09-955-909-9	Sequence 12, Appli
151	16.4	0.7	48	10	US-09-916-940-66	Sequence 66, Appli	C 224	16	0.7	41	10	US-09-816-028A-42	Sequence 42, Appli
152	16.4	0.7	48	10	US-09-918-601-66	Sequence 66, Appli	C 225	16	0.7	41	10	US-09-943-213-3	Sequence 3, Appli
153	16.4	0.7	48	10	US-09-918-601-66	Sequence 66, Appli	C 226	16	0.7	42	9	US-09-942-087A-32	Sequence 32, Appli
C 154	16.4	0.7	48	10	US-09-931-087A-9	Sequence 9, Appli	C 227	16	0.7	42	10	US-09-765-272-428	Sequence 428, App
C 155	16.4	0.7	49	10	US-09-931-087A-35	Sequence 35, Appli	C 228	16	0.7	44	10	US-09-205-658-320	Sequence 320, App
C 156	16.4	0.7	50	9	US-09-978-295A-234	Sequence 234, App	C 229	16	0.7	45	10	US-09-798-058-17	Sequence 17, Appli
157	16.4	0.7	50	10	US-09-504-231A-2947	Sequence 2947, Ap	C 230	16	0.7	45	10	US-09-065-040-3	Sequence 3, Appli
158	16.4	0.7	50	10	US-09-504-231A-2961	Sequence 2961, Ap	C 231	16	0.7	45	10	US-09-827-289-24	Sequence 24, Appli
159	16.4	0.7	50	10	US-09-504-231A-2975	Sequence 2975, Ap	C 232	16	0.7	46	8	US-08-973-391A-12	Sequence 2, Appli
160	16.4	0.7	50	10	US-09-274-553D-2947	Sequence 2947, Ap	C 233	16	0.7	47	10	US-09-922-261-233	Sequence 233, App
161	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 234	16	0.7	48	10	US-09-822-698A-48	Sequence 48, Appli
162	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 235	16	0.7	48	12	US-10-026-389-8	Sequence 8, Appli
163	16.4	0.7	50	10	US-10-036-342-33	Sequence 33, Appli	C 236	16	0.7	49	9	US-09-858-200A-2	Sequence 2, Appli
C 164	16.2	0.7	27	10	US-09-790-417-99	Sequence 9, Appli	C 237	16	0.7	49	10	US-09-738-847-16	Sequence 16, Appli
165	16.2	0.7	27	10	US-09-954-764-2	Sequence 2, Appli	C 238	16	0.7	49	10	US-09-738-847-16	Sequence 16, Appli



239	16	0.7	49	10	US-09-943-215-4	Sequence 4, Appl1	c 312	15.8	0.7	50	10	US-09-274-553D-2973	Sequence 2973, Ap
240	16	0.7	50	10	US-09-740-002-7	Sequence 7, Appl1	c 313	15.8	0.7	50	10	US-09-274-553D-2994	Sequence 2994, Ap
241	16	0.7	50	10	US-09-504-231A-2910	Sequence 2910, Ap	c 314	15.8	0.7	50	10	US-09-274-553D-3028	Sequence 3028, Ap
242	16	0.7	50	10	US-09-504-231A-2932	Sequence 2932, Ap	c 315	15.6	0.7	24	10	US-09-909-446-7	Sequence 7, Appl1
243	16	0.7	50	10	US-09-504-231A-3052	Sequence 3052, Ap	c 316	15.6	0.7	24	10	US-09-909-446-11	Sequence 11, Appl1
244	16	0.7	50	10	US-09-504-231A-3071	Sequence 3071, Ap	c 317	15.6	0.7	24	10	US-09-909-325-7	Sequence 7, Appl1
245	16	0.7	50	10	US-09-504-231A-3085	Sequence 3085, Ap	c 318	15.6	0.7	24	10	US-09-909-325-11	Sequence 11, Appl1
246	16	0.7	50	10	US-09-274-553D-2910	Sequence 2910, Ap	c 319	15.6	0.7	24	10	US-09-909-326-7	Sequence 7, Appl1
247	16	0.7	50	10	US-09-274-553D-2932	Sequence 2932, Ap	c 320	15.6	0.7	24	10	US-09-909-326-11	Sequence 11, Appl1
248	16	0.7	50	10	US-09-274-553D-3052	Sequence 3052, Ap	c 321	15.6	0.7	27	10	US-09-978-730-9	Sequence 9, Appl1
249	16	0.7	50	10	US-09-274-553D-3071	Sequence 3071, Ap	c 322	15.6	0.7	29	9	US-09-863-040-51	Sequence 51, Appl1
250	16	0.7	50	10	US-09-274-553D-3085	Sequence 3085, Ap	c 323	15.6	0.7	30	10	US-09-788-657-1	Sequence 1, Appl1
251	15.8	0.7	22	10	US-09-895-652-30	Sequence 30, Appl1	c 324	15.6	0.7	31	10	US-09-801-274-1579	Sequence 1579, Ap
252	15.8	0.7	27	10	US-09-860-793-24	Sequence 24, Appl1	c 325	15.6	0.7	32	10	US-09-345-790-9	Sequence 9, Appl1
253	15.8	0.7	31	10	US-09-801-274-178	Sequence 178, Ap	c 326	15.6	0.7	35	10	US-09-179-536B-137	Sequence 137, Ap
254	15.8	0.7	31	10	US-09-801-274-1508	Sequence 1508, Ap	c 327	15.6	0.7	35	10	US-09-946-334-5	Sequence 5, Appl1
255	15.8	0.7	31	10	US-09-801-274-1784	Sequence 1784, Ap	c 328	15.6	0.7	35	10	US-09-946-334-6	Sequence 6, Appl1
256	15.8	0.7	31	10	US-09-923-246-57	Sequence 57, Appl1	c 329	15.6	0.7	35	10	US-09-946-334-7	Sequence 7, Appl1
257	15.8	0.7	34	10	US-09-728-466-22	Sequence 22, Appl1	c 330	15.6	0.7	36	10	US-09-946-334-8	Sequence 8, Appl1
258	15.8	0.7	35	10	US-09-728-466-23	Sequence 23, Appl1	c 331	15.6	0.7	36	10	US-09-946-334-9	Sequence 9, Appl1
259	15.8	0.7	35	10	US-09-915-060-12	Sequence 12, Appl1	c 332	15.6	0.7	37	10	US-09-946-334-10	Sequence 10, Appl1
260	15.8	0.7	35	10	US-09-915-060-12	Sequence 12, Appl1	c 333	15.6	0.7	38	10	US-09-946-334-11	Sequence 11, Appl1
261	15.8	0.7	35	10	US-09-915-060-12	Sequence 12, Appl1	c 334	15.6	0.7	39	10	US-09-946-334-12	Sequence 12, Appl1
262	15.8	0.7	36	10	US-09-426-548-155	Sequence 155, App	c 335	15.6	0.7	42	10	US-09-946-334-13	Sequence 13, Appl1
263	15.8	0.7	36	10	US-09-848-164-26	Sequence 26, Appl1	c 336	15.6	0.7	42	10	US-09-946-334-14	Sequence 14, Appl1
264	15.8	0.7	36	10	US-09-848-164-26	Sequence 26, Appl1	c 337	15.6	0.7	43	10	US-09-946-334-15	Sequence 15, Appl1
265	15.8	0.7	38	8	US-08-961-888-38	Sequence 38, Appl1	c 338	15.6	0.7	43	10	US-09-946-334-16	Sequence 16, Appl1
266	15.8	0.7	38	10	US-09-738-968-33	Sequence 33, Appl1	c 339	15.6	0.7	43	10	US-09-946-334-17	Sequence 17, Appl1
267	15.8	0.7	39	10	US-09-765-272-286	Sequence 286, App	c 340	15.6	0.7	43	10	US-09-946-334-18	Sequence 18, Appl1
268	15.8	0.7	40	10	US-09-245-802-18	Sequence 18, Appl1	c 341	15.6	0.7	44	9	US-09-910-518A-5	Sequence 5, Appl1
269	15.8	0.7	40	10	US-09-848-164-39	Sequence 39, Appl1	c 342	15.6	0.7	44	9	US-09-910-518A-6	Sequence 6, Appl1
270	15.8	0.7	41	9	US-10-003-035-62	Sequence 62, Appl1	c 343	15.6	0.7	44	9	US-09-910-518A-7	Sequence 7, Appl1
271	15.8	0.7	41	10	US-09-951-401-45	Sequence 45, Appl1	c 344	15.6	0.7	45	9	US-09-910-518A-8	Sequence 8, Appl1
272	15.8	0.7	41	10	US-09-922-101-45	Sequence 45, Appl1	c 345	15.6	0.7	45	9	US-09-910-518A-9	Sequence 9, Appl1
273	15.8	0.7	42	10	US-09-349-954A-12	Sequence 12, Appl1	c 346	15.6	0.7	45	10	US-09-910-518A-10	Sequence 10, Appl1
274	15.8	0.7	42	10	US-09-907-007-12	Sequence 12, Appl1	c 347	15.6	0.7	45	10	US-09-910-518A-11	Sequence 11, Appl1
275	15.8	0.7	44	10	US-09-899-980A-27	Sequence 27, Appl1	c 348	15.6	0.7	46	10	US-09-910-518A-12	Sequence 12, Appl1
276	15.8	0.7	45	10	US-09-989-861-17	Sequence 17, Appl1	c 349	15.6	0.7	46	10	US-09-910-518A-13	Sequence 13, Appl1
277	15.8	0.7	45	10	US-09-781-902-17	Sequence 17, Appl1	c 350	15.6	0.7	47	9	US-09-910-518A-14	Sequence 14, Appl1
278	15.8	0.7	46	10	US-09-369-735B-4	Sequence 4, Appl1	c 351	15.6	0.7	47	9	US-09-910-518A-15	Sequence 15, Appl1
279	15.8	0.7	46	10	US-09-908-337-6	Sequence 6, Appl1	c 352	15.6	0.7	47	10	US-09-910-518A-16	Sequence 16, Appl1
280	15.8	0.7	46	10	US-09-908-337-6	Sequence 6, Appl1	c 353	15.6	0.7	47	10	US-09-910-518A-17	Sequence 17, Appl1
281	15.8	0.7	47	10	US-09-765-272-391	Sequence 391, App	c 354	15.6	0.7	48	10	US-09-910-518A-18	Sequence 18, Appl1
282	15.8	0.7	47	10	US-09-901-484A-198	Sequence 198, App	c 355	15.6	0.7	48	10	US-09-910-518A-19	Sequence 19, Appl1
283	15.8	0.7	47	10	US-09-901-484A-229	Sequence 229, App	c 356	15.6	0.7	48	10	US-09-910-518A-20	Sequence 20, Appl1
284	15.8	0.7	47	10	US-09-901-484A-240	Sequence 240, App	c 357	15.6	0.7	48	10	US-09-910-518A-21	Sequence 21, Appl1
285	15.8	0.7	47	10	US-09-901-484A-329	Sequence 329, App	c 358	15.6	0.7	49	10	US-09-910-518A-22	Sequence 22, Appl1
286	15.8	0.7	48	9	US-09-760-500A-32	Sequence 32, Appl1	c 359	15.6	0.7	49	10	US-09-910-518A-23	Sequence 23, Appl1
287	15.8	0.7	48	9	US-09-760-500A-64	Sequence 64, Appl1	c 360	15.6	0.7	49	10	US-09-910-518A-24	Sequence 24, Appl1
288	15.8	0.7	48	9	US-09-918-543-18	Sequence 18, Appl1	c 361	15.6	0.7	50	10	US-09-910-518A-25	Sequence 25, Appl1
289	15.8	0.7	48	9	US-09-967-409A-32	Sequence 32, Appl1	c 362	15.6	0.7	50	10	US-09-910-518A-26	Sequence 26, Appl1
290	15.8	0.7	48	9	US-09-967-409A-64	Sequence 64, Appl1	c 363	15.6	0.7	50	10	US-09-910-518A-27	Sequence 27, Appl1
291	15.8	0.7	48	9	US-09-967-409A-32	Sequence 32, Appl1	c 364	15.6	0.7	50	10	US-09-910-518A-28	Sequence 28, Appl1
292	15.8	0.7	48	9	US-09-975-062A-64	Sequence 64, Appl1	c 365	15.6	0.7	50	10	US-09-910-518A-29	Sequence 29, Appl1
293	15.8	0.7	48	9	US-09-976-378A-32	Sequence 32, Appl1	c 366	15.6	0.7	50	10	US-09-910-518A-30	Sequence 30, Appl1
294	15.8	0.7	48	9	US-09-976-378A-64	Sequence 64, Appl1	c 367	15.6	0.7	50	10	US-09-910-518A-31	Sequence 31, Appl1
295	15.8	0.7	48	9	US-09-976-577-32	Sequence 32, Appl1	c 368	15.6	0.7	50	10	US-09-910-518A-32	Sequence 32, Appl1
296	15.8	0.7	48	9	US-09-976-577-64	Sequence 64, Appl1	c 369	15.6	0.7	50	10	US-09-910-518A-33	Sequence 33, Appl1
297	15.8	0.7	48	10	US-09-973-788A-32	Sequence 32, Appl1	c 370	15.6	0.7	50	10	US-09-910-518A-34	Sequence 34, Appl1
298	15.8	0.7	48	10	US-09-973-788A-64	Sequence 64, Appl1	c 371	15.6	0.7	50	10	US-09-910-518A-35	Sequence 35, Appl1
299	15.8	0.7	48	10	US-09-923-625-32	Sequence 32, Appl1	c 372	15.6	0.7	50	10	US-09-910-518A-36	Sequence 36, Appl1
300	15.8	0.7	48	10	US-09-973-638A-32	Sequence 32, Appl1	c 373	15.6	0.7	50	10	US-09-910-518A-37	Sequence 37, Appl1
301	15.8	0.7	48	10	US-09-973-638A-64	Sequence 64, Appl1	c 374	15.6	0.7	50	10	US-09-910-518A-38	Sequence 38, Appl1
302	15.8	0.7	48	10	US-09-974-007-32	Sequence 32, Appl1	c 375	15.6	0.7	50	10	US-09-910-518A-39	Sequence 39, Appl1
303	15.8	0.7	48	10	US-09-974-007-64	Sequence 64, Appl1	c 376	15.6	0.7	50	10	US-09-910-518A-40	Sequence 40, Appl1
304	15.8	0.7	48	10	US-09-976-617A-32	Sequence 32, Appl1	c 377	15.6	0.7	50	10	US-09-910-518A-41	Sequence 41, Appl1
305	15.8	0.7	48	10	US-09-976-617A-64	Sequence 64, Appl1	c 378	15.6	0.7	50	10	US-09-910-518A-42	Sequence 42, Appl1
306	15.8	0.7	48	10	US-09-961-949A-32	Sequence 32, Appl1	c 379	15.6	0.7	50	10	US-09-910-518A-43	Sequence 43, Appl1
307	15.8	0.7	48	10	US-09-961-949A-64	Sequence 64, Appl1	c 380	15.6	0.7	50	10	US-09-910-518A-44	Sequence 44, Appl1
308	15.8	0.7	48	10	US-09-978-295A-83	Sequence 83, Appl1	c 381	15.6	0.7	50	10	US-09-910-518A-45	Sequence 45, Appl1
309	15.8	0.7	50	10	US-09-504-231A-2973	Sequence 2973, Ap	c 382	15.6	0.7	50	10	US-09-910-518A-46	Sequence 46, Appl1
310	15.8	0.7	50	10	US-09-504-231A-2994	Sequence 2994, Ap	c 383	15.6	0.7	50	10	US-09-910-518A-47	Sequence 47, Appl1
311	15.8	0.7	50	10	US-09-504-231A-3028	Sequence 3028, Ap	c 384	15.4	0.7	25	10	US-09-866-108-12651	Sequence 12651, A

C 385	15.4	0.7	25	10	US-09-866-108-13695	Sequence 13695, A	C 458	15.4	0.7	50	10	US-09-504-231A-2987	Sequence 2987, Ap
C 386	15.4	0.7	25	10	US-09-866-108-13696	Sequence 13696, A	C 459	15.4	0.7	50	10	US-09-504-231A-2991	Sequence 2991, Ap
C 387	15.4	0.7	25	10	US-09-866-108-14966	Sequence 14966, A	C 460	15.4	0.7	50	10	US-09-504-231A-3014	Sequence 3014, Ap
C 388	15.4	0.7	25	10	US-09-866-108-15544	Sequence 15544, A	C 461	15.4	0.7	50	10	US-09-504-231A-3026	Sequence 3026, Ap
C 389	15.4	0.7	25	10	US-09-871-579-13	Sequence 13, Appl	C 462	15.4	0.7	50	10	US-09-504-231A-3096	Sequence 3096, Ap
C 390	15.4	0.7	25	10	US-09-843-007-4	Sequence 4, Appl	C 463	15.4	0.7	50	10	US-09-867-193-9	Sequence 9, Appl
C 391	15.4	0.7	27	10	US-09-334-923A-44	Sequence 44, Appl	C 464	15.4	0.7	50	10	US-09-274-553D-2915	Sequence 2915, Appl
C 392	15.4	0.7	27	10	US-09-975-901-8	Sequence 8, Appl	C 465	15.4	0.7	50	10	US-09-274-553D-2948	Sequence 2948, Ap
C 393	15.4	0.7	27	10	US-09-975-901-12	Sequence 12, Appl	C 466	15.4	0.7	50	10	US-09-274-553D-2971	Sequence 2971, Ap
C 394	15.4	0.7	27	10	US-09-334-954A-44	Sequence 44, Appl	C 467	15.4	0.7	50	10	US-09-274-553D-2987	Sequence 2987, Ap
C 395	15.4	0.7	27	10	US-09-333-966-10	Sequence 10, Appl	C 468	15.4	0.7	50	10	US-09-274-553D-2991	Sequence 2991, Ap
C 396	15.4	0.7	29	10	US-09-756-095-93	Sequence 93, Appl	C 469	15.4	0.7	50	10	US-09-274-553D-3014	Sequence 3014, Ap
C 397	15.4	0.7	30	10	US-09-952-168-62	Sequence 62, Appl	C 470	15.4	0.7	50	10	US-09-274-553D-3026	Sequence 3026, Ap
C 398	15.4	0.7	31	10	US-09-272-162-5	Sequence 5, Appl	C 471	15.4	0.7	50	10	US-09-274-553D-3096	Sequence 3096, Ap
C 399	15.4	0.7	31	10	US-09-801-274-255	Sequence 255, App	C 472	15.2	0.7	23	10	US-09-868-899-25	Sequence 3096, Ap
C 400	15.4	0.7	31	10	US-09-801-274-1260	Sequence 1260, Ap	C 473	15.2	0.7	24	10	US-09-868-899-25	Sequence 3096, Ap
C 401	15.4	0.7	32	10	US-09-894-698-1311	Sequence 1311, Ap	C 474	15.2	0.7	24	10	US-09-868-899-25	Sequence 3096, Ap
C 402	15.4	0.7	33	10	US-09-333-966-10	Sequence 10, Appl	C 475	15.2	0.7	28	10	US-09-904-116-6	Sequence 14, Appl
C 403	15.4	0.7	33	10	US-09-333-966-13	Sequence 13, Appl	C 476	15.2	0.7	28	10	US-09-904-116-6	Sequence 14, Appl
C 404	15.4	0.7	33	10	US-09-333-966-16	Sequence 16, Appl	C 477	15.2	0.7	29	10	US-09-887-576-416	Sequence 10, Appl
C 405	15.4	0.7	33	12	US-10-108-280-2	Sequence 2, Appl	C 478	15.2	0.7	30	9	US-09-944-413-109	Sequence 416, App
C 406	15.4	0.7	34	9	US-09-826-025-22	Sequence 22, Appl	C 479	15.2	0.7	30	10	US-09-771-425-3	Sequence 109, App
C 407	15.4	0.7	34	10	US-09-765-272-250	Sequence 250, App	C 480	15.2	0.7	30	10	US-09-866-028-109	Sequence 3, Appl
C 408	15.4	0.7	34	10	US-09-765-272-293	Sequence 293, App	C 481	15.2	0.7	30	10	US-09-944-449-109	Sequence 109, App
C 409	15.4	0.7	35	10	US-09-920-552-105	Sequence 105, App	C 482	15.2	0.7	30	10	US-09-944-457-109	Sequence 109, App
C 410	15.4	0.7	35	12	US-10-139-262-30	Sequence 30, Appl	C 483	15.2	0.7	30	10	US-09-945-587-109	Sequence 109, App
C 411	15.4	0.7	36	10	US-09-504-231A-2341	Sequence 2341, Ap	C 484	15.2	0.7	30	10	US-09-945-587-109	Sequence 109, App
C 412	15.4	0.7	36	10	US-09-765-272-280	Sequence 280, App	C 485	15.2	0.7	30	10	US-09-944-396-109	Sequence 109, App
C 413	15.4	0.7	36	10	US-09-274-553D-2341	Sequence 2341, Ap	C 486	15.2	0.7	30	10	US-09-944-396-109	Sequence 109, App
C 414	15.4	0.7	37	10	US-09-755-665-108	Sequence 108, App	C 487	15.2	0.7	30	10	US-09-944-432-109	Sequence 109, App
C 415	15.4	0.7	38	10	US-09-765-272-441	Sequence 441, App	C 488	15.2	0.7	30	10	US-09-944-432-109	Sequence 109, App
C 416	15.4	0.7	38	10	US-09-944-243-2	Sequence 2, Appl	C 489	15.2	0.7	30	10	US-09-944-654-109	Sequence 109, App
C 417	15.4	0.7	38	10	US-09-874-389-15	Sequence 15, Appl	C 490	15.2	0.7	30	10	US-09-943-851A-109	Sequence 109, App
C 418	15.4	0.7	40	10	US-09-951-401-68	Sequence 68, Appl	C 491	15.2	0.7	31	9	US-10-029-905-7	Sequence 109, App
C 419	15.4	0.7	41	10	US-09-922-101-68	Sequence 68, Appl	C 492	15.2	0.7	31	10	US-09-801-274-990	Sequence 990, App
C 420	15.4	0.7	41	10	US-09-955-462A-1	Sequence 1, Appl	C 493	15.2	0.7	31	10	US-09-801-274-1451	Sequence 1451, Ap
C 421	15.4	0.7	42	9	US-09-966-140-32	Sequence 32, Appl	C 494	15.2	0.7	31	10	US-09-804-898-4	Sequence 4, Appl
C 422	15.4	0.7	44	9	US-09-793-139-36	Sequence 36, Appl	C 495	15.2	0.7	31	10	US-09-895-263-6	Sequence 6, Appl
C 423	15.4	0.7	44	9	US-09-793-139-37	Sequence 37, Appl	C 496	15.2	0.7	33	8	US-08-978-633-14	Sequence 14, Appl
C 424	15.4	0.7	44	10	US-09-818-879-36	Sequence 36, Appl	C 497	15.2	0.7	33	8	US-08-978-633-14	Sequence 14, Appl
C 425	15.4	0.7	44	10	US-09-818-879-37	Sequence 37, Appl	C 498	15.2	0.7	33	8	US-08-978-633-14	Sequence 14, Appl
C 426	15.4	0.7	44	10	US-09-211-755B-36	Sequence 36, Appl	C 499	15.2	0.7	33	8	US-08-978-633-14	Sequence 14, Appl
C 427	15.4	0.7	44	10	US-09-211-755B-37	Sequence 37, Appl	C 500	15.2	0.7	33	10	US-09-816-531A-27	Sequence 27, Appl
C 428	15.4	0.7	45	10	US-09-838-386-17	Sequence 17, Appl	C 501	15.2	0.7	34	10	US-09-923-246-27	Sequence 27, Appl
C 429	15.4	0.7	45	10	US-09-838-386-18	Sequence 18, Appl	C 502	15.2	0.7	35	9	US-09-923-246-27	Sequence 27, Appl
C 430	15.4	0.7	45	10	US-09-867-274-19	Sequence 19, Appl	C 503	15.2	0.7	35	10	US-09-275-805-4	Sequence 4, Appl
C 431	15.4	0.7	46	10	US-09-827-289-25	Sequence 25, Appl	C 504	15.2	0.7	35	10	US-09-732-561-12	Sequence 12, Appl
C 432	15.4	0.7	46	10	US-09-827-289-26	Sequence 26, Appl	C 505	15.2	0.7	36	8	US-08-424-550B-625	Sequence 625, Appl
C 433	15.4	0.7	47	10	US-09-151-450-9	Sequence 9, Appl	C 506	15.2	0.7	36	10	US-09-943-215-7	Sequence 7, Appl
C 434	15.4	0.7	47	10	US-09-901-484A-196	Sequence 196, App	C 507	15.2	0.7	36	10	US-09-943-215-7	Sequence 7, Appl
C 435	15.4	0.7	47	10	US-09-901-484A-244	Sequence 244, App	C 508	15.2	0.7	37	9	US-09-840-243B-3	Sequence 235, App
C 436	15.4	0.7	47	10	US-09-901-484A-252	Sequence 252, App	C 509	15.2	0.7	38	10	US-09-973-451-32	Sequence 32, Appl
C 437	15.4	0.7	48	9	US-09-760-500A-29	Sequence 29, Appl	C 510	15.2	0.7	39	10	US-09-727-311-26	Sequence 275, App
C 438	15.4	0.7	48	9	US-09-967-409A-29	Sequence 29, Appl	C 511	15.2	0.7	39	10	US-09-765-272-25	Sequence 275, App
C 439	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 512	15.2	0.7	39	10	US-09-774-414-20	Sequence 20, Appl
C 440	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 513	15.2	0.7	41	10	US-09-782-361-22	Sequence 22, Appl
C 441	15.4	0.7	48	9	US-09-976-378A-29	Sequence 29, Appl	C 514	15.2	0.7	41	10	US-09-951-401-62	Sequence 62, Appl
C 442	15.4	0.7	48	9	US-09-976-378A-29	Sequence 29, Appl	C 515	15.2	0.7	41	10	US-09-951-401-62	Sequence 62, Appl
C 443	15.4	0.7	48	10	US-09-217-268B-16	Sequence 16, Appl	C 516	15.2	0.7	42	10	US-09-878-766A-10	Sequence 10, Appl
C 444	15.4	0.7	48	10	US-09-978-274A-11	Sequence 11, Appl	C 517	15.2	0.7	42	10	US-09-774-414-28	Sequence 28, Appl
C 445	15.4	0.7	48	10	US-09-973-788A-29	Sequence 29, Appl	C 518	15.2	0.7	42	10	US-09-779-081-3	Sequence 3, Appl
C 446	15.4	0.7	48	10	US-09-923-625-29	Sequence 29, Appl	C 519	15.2	0.7	42	10	US-09-774-414-20	Sequence 20, Appl
C 447	15.4	0.7	48	10	US-09-973-638A-29	Sequence 29, Appl	C 520	15.2	0.7	42	12	US-10-053-349-3	Sequence 3, Appl
C 448	15.4	0.7	48	10	US-09-974-007-29	Sequence 29, Appl	C 521	15.2	0.7	43	10	US-09-993-170-21	Sequence 21, Appl
C 449	15.4	0.7	48	10	US-09-976-617A-29	Sequence 29, Appl	C 522	15.2	0.7	44	10	US-09-993-170-21	Sequence 21, Appl
C 450	15.4	0.7	49	10	US-09-961-949A-29	Sequence 29, Appl	C 523	15.2	0.7	44	10	US-09-932-679-28	Sequence 28, Appl
C 451	15.4	0.7	49	10	US-09-978-274A-14	Sequence 14, Appl	C 524	15.2	0.7	44	10	US-09-844-493-22	Sequence 22, Appl
C 452	15.4	0.7	50	9	US-09-978-295A-408	Sequence 408, App	C 525	15.2	0.7	44	10	US-09-844-501-22	Sequence 22, Appl
C 453	15.4	0.7	50	10	US-09-790-417-279	Sequence 279, App	C 526	15.2	0.7	44	10	US-09-988-889-58	Sequence 58, Appl
C 454	15.4	0.7	50	10	US-09-815-343-1012	Sequence 1012, App	C 527	15.2	0.7	44	10	US-09-988-889-58	Sequence 58, Appl
C 455	15.4	0.7	50	10	US-09-504-231A-2915	Sequence 2915, Ap	C 528	15.2	0.7	46	10	US-09-844-265-22	Sequence 22, Appl
C 456	15.4	0.7	50	10	US-09-504-231A-2948	Sequence 2948, Ap	C 529	15.2	0.7	46	10	US-09-844-265-22	Sequence 22, Appl
C 457	15.4	0.7	50	10	US-09-504-231A-2971	Sequence 2971, Ap	C 530	15.2	0.7	46	10	US-09-835-147-21	Sequence 21, Appl

531	15.2	0.7	46	10	US-09-827-289-22	Sequence 22, Appl	604	15	0.6	25	10	US-09-866-108-15408	Sequence 15408, A
C 532	15.2	0.7	47	9	US-09-995-749A-9	Sequence 9, Appl1	605	15	0.6	25	10	US-09-263-959-876	Sequence 876, App
C 533	15.2	0.7	47	10	US-09-822-250-35	Sequence 35, Appl	606	15	0.6	25	10	US-09-263-689-46	Sequence 46, Appl
534	15.2	0.7	47	10	US-09-817-014-19	Sequence 19, Appl	607	15	0.6	26	10	US-09-179-536B-134	Sequence 134, App
535	15.2	0.7	47	10	US-09-901-484A-220	Sequence 220, App	608	15	0.6	27	12	US-10-139-662-15	Sequence 15, Appl
536	15.2	0.7	47	10	US-09-901-484A-235	Sequence 235, App	609	15	0.6	28	12	US-10-005-073-4	Sequence 4, Appl1
C 537	15.2	0.7	47	10	US-09-901-484A-284	Sequence 284, App	610	15	0.6	28	12	US-10-005-073-6	Sequence 6, Appl1
C 538	15.2	0.7	47	10	US-09-901-484A-312	Sequence 312, App	611	15	0.6	29	10	US-09-179-536B-133	Sequence 133, App
C 539	15.2	0.7	48	9	US-09-905-291A-357	Sequence 357, App	612	15	0.6	29	10	US-09-179-536B-135	Sequence 135, App
C 540	15.2	0.7	48	10	US-09-284-665A-20	Sequence 20, Appl	C 613	15	0.6	30	9	US-09-924-097-10	Sequence 10, Appl
C 541	15.2	0.7	48	10	US-09-810-502-29	Sequence 29, Appl	614	15	0.6	30	10	US-09-825-301-61	Sequence 61, Appl
C 542	15.2	0.7	48	10	US-09-909-320-357	Sequence 357, App	615	15	0.6	30	10	US-09-989-441-15	Sequence 15, Appl
C 543	15.2	0.7	48	10	US-09-909-088B-357	Sequence 357, App	616	15	0.6	31	10	US-09-801-274-1636	Sequence 1636, App
C 544	15.2	0.7	49	10	US-09-900-062-43	Sequence 43, Appl	617	15	0.6	31	10	US-09-179-536B-139	Sequence 139, App
545	15.2	0.7	50	9	US-09-996-956-6	Sequence 6, Appl1	618	15	0.6	31	10	US-09-905-173-8	Sequence 8, Appl1
546	15.2	0.7	50	9	US-09-905-291A-270	Sequence 270, App	619	15	0.6	32	9	US-09-319-264-1	Sequence 1, Appl1
C 547	15.2	0.7	50	9	US-09-992-598-50	Sequence 50, Appl	620	15	0.6	32	10	US-09-814-786-37	Sequence 37, Appl
C 548	15.2	0.7	50	10	US-09-790-417-279	Sequence 279, App	C 621	15	0.6	32	10	US-09-804-682-89	Sequence 89, Appl
549	15.2	0.7	50	10	US-09-790-417-280	Sequence 280, App	622	15	0.6	32	10	US-09-804-682-92	Sequence 92, Appl
C 550	15.2	0.7	50	10	US-09-504-231A-2923	Sequence 2923, App	C 623	15	0.6	33	10	US-09-426-548-15	Sequence 15, Appl
C 551	15.2	0.7	50	10	US-09-504-231A-2936	Sequence 2936, App	624	15	0.6	33	10	US-09-930-251-10	Sequence 10, Appl
C 552	15.2	0.7	50	10	US-09-504-231A-2953	Sequence 2953, App	C 625	15	0.6	33	10	US-09-804-682-86	Sequence 86, Appl
C 553	15.2	0.7	50	10	US-09-504-231A-2972	Sequence 2972, App	626	15	0.6	33	10	US-09-804-682-93	Sequence 93, Appl
C 554	15.2	0.7	50	10	US-09-504-231A-3038	Sequence 3038, App	627	15	0.6	33	10	US-09-263-689-47	Sequence 47, Appl
C 555	15.2	0.7	50	10	US-09-504-231A-3042	Sequence 3042, App	628	15	0.6	33	10	US-09-263-689-54	Sequence 54, Appl
C 556	15.2	0.7	50	10	US-09-504-231A-3049	Sequence 3049, App	C 629	15	0.6	34	9	US-09-771-009-27	Sequence 27, Appl
C 557	15.2	0.7	50	10	US-09-504-231A-3059	Sequence 3059, App	630	15	0.6	34	10	US-09-766-095-36	Sequence 36, Appl
C 558	15.2	0.7	50	10	US-09-504-231A-3084	Sequence 3084, App	631	15	0.6	34	10	US-09-925-365B-7	Sequence 7, Appl1
C 559	15.2	0.7	50	10	US-09-504-231A-3091	Sequence 3091, App	C 632	15	0.6	34	10	US-09-884-814-3	Sequence 3, Appl1
C 560	15.2	0.7	50	10	US-09-504-231A-3095	Sequence 3095, App	633	15	0.6	35	10	US-09-790-309-15	Sequence 15, Appl
C 561	15.2	0.7	50	10	US-09-504-231A-3107	Sequence 3107, App	C 634	15	0.6	35	10	US-09-915-060-14	Sequence 14, Appl
562	15.2	0.7	50	10	US-09-841-132-207	Sequence 207, App	C 635	15	0.6	35	10	US-09-915-060-16	Sequence 16, Appl
C 563	15.2	0.7	50	10	US-09-989-722-50	Sequence 50, Appl	C 636	15	0.6	35	10	US-09-915-060-16	Sequence 16, Appl
C 564	15.2	0.7	50	10	US-09-989-722-50	Sequence 50, Appl	C 637	15	0.6	36	10	US-09-835-147-19	Sequence 7, Appl1
C 565	15.2	0.7	50	10	US-09-989-729-50	Sequence 50, Appl	638	15	0.6	37	10	US-09-120-044-7	Sequence 7, Appl1
C 566	15.2	0.7	50	10	US-09-989-727-50	Sequence 50, Appl	C 639	15	0.6	37	10	US-09-952-572-6	Sequence 6, Appl1
C 567	15.2	0.7	50	10	US-09-274-553D-2923	Sequence 2923, App	C 640	15	0.6	37	10	US-09-948-41A-1	Sequence 1, Appl1
C 568	15.2	0.7	50	10	US-09-274-553D-2936	Sequence 2936, App	641	15	0.6	38	9	US-09-818-879-33	Sequence 33, Appl
C 569	15.2	0.7	50	10	US-09-274-553D-2953	Sequence 2953, App	642	15	0.6	38	10	US-09-179-536B-136	Sequence 136, App
570	15.2	0.7	50	10	US-09-274-553D-2972	Sequence 2972, App	643	15	0.6	38	10	US-09-211-755B-13	Sequence 33, Appl
C 571	15.2	0.7	50	10	US-09-274-553D-3038	Sequence 3038, App	644	15	0.6	38	10	US-09-766-095-37	Sequence 37, Appl
C 572	15.2	0.7	50	10	US-09-274-553D-3042	Sequence 3042, App	C 645	15	0.6	38	10	US-09-766-095-117	Sequence 117, App
C 573	15.2	0.7	50	10	US-09-274-553D-3049	Sequence 3049, App	C 646	15	0.6	38	10	US-09-885-478-11	Sequence 11, Appl
C 574	15.2	0.7	50	10	US-09-274-553D-3059	Sequence 3059, App	647	15	0.6	38	10	US-09-885-478-11	Sequence 11, Appl
C 575	15.2	0.7	50	10	US-09-274-553D-3084	Sequence 3084, App	C 648	15	0.6	38	10	US-09-888-049-10	Sequence 10, Appl
C 576	15.2	0.7	50	10	US-09-274-553D-3091	Sequence 3091, App	649	15	0.6	38	10	US-09-870-122-15	Sequence 15, Appl
C 577	15.2	0.7	50	10	US-09-274-553D-3095	Sequence 3095, App	C 650	15	0.6	38	12	US-10-007-448-3	Sequence 3, Appl1
C 578	15.2	0.7	50	10	US-09-274-553D-3107	Sequence 3107, App	C 651	15	0.6	39	9	US-09-771-009-24	Sequence 24, Appl
C 579	15.2	0.7	50	10	US-09-989-731-50	Sequence 50, Appl	C 652	15	0.6	39	10	US-09-753-436-109	Sequence 109, App
C 580	15.2	0.7	50	10	US-09-989-733-50	Sequence 50, Appl	C 653	15	0.6	39	10	US-09-987-456-144	Sequence 144, App
C 581	15.2	0.7	50	10	US-09-989-733-50	Sequence 50, Appl	C 654	15	0.6	39	10	US-09-987-456-144	Sequence 144, App
582	15.2	0.7	50	10	US-09-909-320-270	Sequence 270, App	C 655	15	0.6	39	12	US-10-066-151-62	Sequence 62, Appl
C 583	15.2	0.7	50	10	US-09-909-442-50	Sequence 50, Appl	C 656	15	0.6	40	9	US-09-996-140-28	Sequence 28, Appl
C 584	15.2	0.7	50	10	US-09-911-163-50	Sequence 50, Appl	657	15	0.6	40	10	US-09-765-272-253	Sequence 253, App
C 585	15.2	0.7	50	10	US-09-933-604-50	Sequence 50, Appl	658	15	0.6	40	10	US-09-842-154-20	Sequence 20, Appl
C 586	15.2	0.7	50	10	US-09-930-456-50	Sequence 50, Appl	659	15	0.6	40	10	US-09-924-154-10	Sequence 10, Appl
C 587	15.2	0.7	50	10	US-09-989-721-50	Sequence 50, Appl	660	15	0.6	40	10	US-09-910-120-10	Sequence 10, Appl
C 588	15.2	0.7	50	10	US-09-909-088B-270	Sequence 270, App	661	15	0.6	41	10	US-09-920-581-9	Sequence 9, Appl1
C 589	15	0.6	21	10	US-09-888-243-10	Sequence 10, Appl	662	15	0.6	42	9	US-09-771-009-26	Sequence 26, Appl
C 590	15	0.6	23	10	US-09-927-602-35	Sequence 35, Appl	C 663	15	0.6	42	9	US-09-887-880-15	Sequence 15, Appl
C 591	15	0.6	23	10	US-09-777-430A-18	Sequence 18, Appl	664	15	0.6	42	9	US-09-978-295A-243	Sequence 243, App
C 592	15	0.6	24	10	US-09-923-684-11	Sequence 11, Appl	665	15	0.6	42	10	US-09-904-568-12	Sequence 12, Appl
C 593	15	0.6	24	10	US-09-779-307-42	Sequence 42, Appl	666	15	0.6	42	10	US-09-824-568-3	Sequence 3, Appl1
594	15	0.6	25	10	US-09-866-108-12652	Sequence 12652, A	667	15	0.6	43	10	US-09-732-561-11	Sequence 11, Appl
595	15	0.6	25	10	US-09-866-108-13692	Sequence 13692, A	668	15	0.6	44	10	US-09-732-348-9	Sequence 9, Appl1
C 596	15	0.6	25	10	US-09-866-108-14867	Sequence 14867, A	C 669	15	0.6	45	9	US-09-292-973-14	Sequence 14, Appl
597	15	0.6	25	10	US-09-866-108-14868	Sequence 14868, A	670	15	0.6	45	9	US-09-729-520-4	Sequence 4, Appl1
598	15	0.6	25	10	US-09-866-108-14869	Sequence 14869, A	671	15	0.6	45	9	US-10-008-620-4	Sequence 4, Appl1
599	15	0.6	25	10	US-09-866-108-14870	Sequence 14870, A	C 672	15	0.6	45	10	US-09-828-592-5	Sequence 5, Appl1
600	15	0.6	25	10	US-09-866-108-14871	Sequence 14871, A	C 673	15	0.6	45	10	US-09-827-289-18	Sequence 18, Appl
601	15	0.6	25	10	US-09-866-108-14872	Sequence 14872, A	C 674	15	0.6	45	10	US-09-818-066-32	Sequence 32, Appl
602	15	0.6	25	10	US-09-866-108-14873	Sequence 14873, A	C 675	15	0.6	45	10	US-09-848-164-104	Sequence 104, App
603	15	0.6	25	10	US-09-866-108-15405	Sequence 15405, A	C 676	15	0.6	46	10	US-09-320-337-38	Sequence 38, Appl

677	15	0.6	46	10	US-09-827-289-20	Sequence 20, Appl	750	14.8	0.6	29	12	US-10-040-916-64	Sequence 64, Appl
678	15	0.6	46	10	US-09-932-679-22	Sequence 22, Appl	751	14.8	0.6	30	10	US-09-725-735A-9	Sequence 9, Appl1
679	15	0.6	47	10	US-09-804-682-108	Sequence 108, App	752	14.8	0.6	30	10	US-09-853-053-4	Sequence 4, Appl1
680	15	0.6	47	10	US-09-901-484A-210	Sequence 210, App	753	14.8	0.6	30	10	US-09-853-053-5	Sequence 5, Appl1
681	15	0.6	47	10	US-09-901-484A-219	Sequence 219, App	754	14.8	0.6	30	10	US-09-853-053-12	Sequence 12, Appl
682	15	0.6	47	10	US-09-901-484A-231	Sequence 231, App	755	14.8	0.6	30	10	US-09-760-574-5	Sequence 5, Appl1
683	15	0.6	47	10	US-09-901-484A-247	Sequence 247, App	756	14.8	0.6	30	10	US-09-777-40A-21	Sequence 21, Appl
684	15	0.6	47	10	US-09-901-484A-308	Sequence 308, App	757	14.8	0.6	31	10	US-09-801-274-673	Sequence 673, App
685	15	0.6	47	10	US-09-901-484A-311	Sequence 311, App	758	14.8	0.6	31	10	US-09-801-274-1346	Sequence 1346, App
686	15	0.6	48	10	US-09-755-747A-1	Sequence 1, Appl1	759	14.8	0.6	31	10	US-09-801-274-1625	Sequence 1625, App
687	15	0.6	48	10	US-09-351-819-2	Sequence 16, Appl	761	14.8	0.6	31	10	US-09-801-274-1771	Sequence 1771, App
688	15	0.6	48	12	US-10-091-085-16	Sequence 91, Appl	762	14.8	0.6	31	10	US-09-885-478-19	Sequence 18, Appl
689	15	0.6	49	9	US-09-987-107-91	Sequence 238, App	763	14.8	0.6	32	8	US-08-945-038-17	Sequence 17, Appl
690	15	0.6	49	9	US-09-905-291A-380	Sequence 380, App	764	14.8	0.6	32	12	US-10-013-718-1	Sequence 1, Appl1
691	15	0.6	49	9	US-09-905-291A-388	Sequence 27, App	765	14.8	0.6	33	9	US-10-106-092-9	Sequence 9, Appl1
692	15	0.6	49	10	US-09-781-902-27	Sequence 43, Appl	766	14.8	0.6	33	10	US-09-927-886-16	Sequence 16, Appl
693	15	0.6	49	10	US-09-900-062-43	Sequence 238, App	767	14.8	0.6	33	10	US-09-792-439-6	Sequence 6, Appl1
694	15	0.6	49	10	US-09-909-320-338	Sequence 380, App	768	14.8	0.6	34	10	US-09-784-982-9	Sequence 9, Appl1
695	15	0.6	49	10	US-09-909-320-380	Sequence 12, Appl	769	14.8	0.6	34	10	US-09-419-305-9	Sequence 9, Appl1
696	15	0.6	49	10	US-09-758-525A-12	Sequence 1, Appl1	770	14.8	0.6	34	10	US-09-931-186-13	Sequence 13, Appl
697	15	0.6	49	10	US-09-944-243-1	Sequence 238, App	771	14.8	0.6	34	10	US-09-931-186-24	Sequence 24, Appl
698	15	0.6	49	10	US-09-909-088B-238	Sequence 380, App	772	14.8	0.6	34	10	US-09-931-186-24	Sequence 803, App
699	15	0.6	49	10	US-09-909-088B-380	Sequence 9, Appl1	773	14.8	0.6	34	12	US-10-045-428A-11	Sequence 11, Appl
700	15	0.6	50	9	US-09-801-371A-9	Sequence 277, App	774	14.8	0.6	35	8	US-08-961-888-31	Sequence 31, Appl
701	15	0.6	50	10	US-09-790-417-277	Sequence 278, App	775	14.8	0.6	35	9	US-09-811-088-13	Sequence 13, Appl
702	15	0.6	50	10	US-09-790-417-278	Sequence 280, App	776	14.8	0.6	35	10	US-09-727-311-22	Sequence 22, Appl
703	15	0.6	50	10	US-09-790-417-280	Sequence 3003, App	777	14.8	0.6	35	10	US-09-732-661-2	Sequence 2, Appl1
704	15	0.6	50	10	US-09-504-231A-3003	Sequence 3019, App	778	14.8	0.6	35	10	US-09-732-661-2	Sequence 27, Appl
705	15	0.6	50	10	US-09-504-231A-3019	Sequence 3029, App	779	14.8	0.6	35	10	US-09-971-309-36	Sequence 36, Appl
706	15	0.6	50	10	US-09-504-231A-3029	Sequence 3047, App	780	14.8	0.6	36	8	US-08-786-531B-7	Sequence 7, Appl1
707	15	0.6	50	10	US-09-504-231A-3047	Sequence 3062, App	781	14.8	0.6	36	8	US-08-424-550B-641	Sequence 64, App
708	15	0.6	50	10	US-09-504-231A-3062	Sequence 3062, App	782	14.8	0.6	36	10	US-09-426-548-112	Sequence 112, App
709	15	0.6	50	10	US-09-504-231A-3065	Sequence 3065, App	783	14.8	0.6	36	10	US-09-426-548-115	Sequence 155, App
710	15	0.6	50	10	US-09-504-231A-3066	Sequence 3085, App	784	14.8	0.6	36	10	US-09-735-450-9	Sequence 9, Appl1
711	15	0.6	50	10	US-09-504-231A-3085	Sequence 1, Appl1	785	14.8	0.6	36	10	US-09-759-352-11	Sequence 11, Appl
712	15	0.6	50	10	US-09-909-496-1	Sequence 4, Appl1	786	14.8	0.6	36	10	US-09-903-456-105	Sequence 105, App
713	15	0.6	50	10	US-09-909-496-10	Sequence 10, Appl1	787	14.8	0.6	37	12	US-10-127-733-7	Sequence 7, Appl1
714	15	0.6	50	10	US-09-909-496-10	Sequence 3003, App	788	14.8	0.6	37	9	US-09-992-598-463	Sequence 463, App
715	15	0.6	50	10	US-09-924-553D-3003	Sequence 3019, App	789	14.8	0.6	37	10	US-09-989-722-463	Sequence 463, App
716	15	0.6	50	10	US-09-274-553D-3019	Sequence 3029, App	790	14.8	0.6	37	10	US-09-989-723-463	Sequence 463, App
717	15	0.6	50	10	US-09-274-553D-3029	Sequence 3047, App	791	14.8	0.6	37	10	US-09-989-727-463	Sequence 463, App
718	15	0.6	50	10	US-09-274-553D-3060	Sequence 3060, App	792	14.8	0.6	37	10	US-09-989-727-463	Sequence 463, App
719	15	0.6	50	10	US-09-274-553D-3066	Sequence 3066, App	793	14.8	0.6	37	10	US-09-989-731-463	Sequence 463, App
720	15	0.6	50	10	US-09-274-553D-3085	Sequence 3085, App	794	14.8	0.6	37	10	US-09-989-732-463	Sequence 463, App
721	15	0.6	50	10	US-09-776-529A-3	Sequence 2759, App	795	14.8	0.6	37	10	US-09-991-073-463	Sequence 463, App
722	15	0.6	50	10	US-09-776-529A-15	Sequence 15, Appl	796	14.8	0.6	37	10	US-09-990-442-463	Sequence 463, App
723	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	797	14.8	0.6	37	10	US-09-991-163-463	Sequence 463, App
724	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	798	14.8	0.6	37	10	US-09-991-163-463	Sequence 463, App
725	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	799	14.8	0.6	37	10	US-09-993-604-463	Sequence 463, App
726	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	800	14.8	0.6	37	10	US-09-990-456-463	Sequence 463, App
727	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	801	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
728	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	802	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
729	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	803	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
730	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	804	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
731	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	805	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
732	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	806	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
733	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	807	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
734	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	808	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
735	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	809	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
736	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	810	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
737	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	811	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
738	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	812	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
739	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	813	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
740	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	814	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
741	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	815	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
742	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	816	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
743	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	817	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
744	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	818	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
745	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	819	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
746	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	820	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
747	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	821	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
748	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	822	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
749	15	0.6	50	10	US-09-811-047-1	Sequence 15, Appl	823	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App

C 823	14.8	0.6	40	10	US-09-990-456-324	Sequence 324, App	896	14.8	0.6	50	10	US-09-989-731-144	Sequence 144, App
C 824	14.8	0.6	40	10	US-09-989-721-324	Sequence 324, App	897	14.8	0.6	50	10	US-09-264-4688-7	Sequence 7, App1
C 825	14.8	0.6	40	10	US-09-263-959-221	Sequence 221, App	898	14.8	0.6	50	10	US-09-912-787-19	Sequence 19, App1
C 826	14.8	0.6	41	10	US-09-765-272-331	Sequence 331, App	899	14.8	0.6	50	10	US-09-989-732-144	Sequence 144, App
C 827	14.8	0.6	41	10	US-09-908-855-31	Sequence 31, App1	900	14.8	0.6	50	10	US-09-991-073-144	Sequence 144, App
C 828	14.8	0.6	41	10	US-09-823-829-45	Sequence 45, App1	901	14.8	0.6	50	10	US-09-909-320-79	Sequence 79, App1
C 829	14.8	0.6	42	10	US-09-810-502-21	Sequence 21, App1	902	14.8	0.6	50	10	US-09-990-442-144	Sequence 144, App
C 830	14.8	0.6	42	10	US-09-826-312-16	Sequence 16, App1	903	14.8	0.6	50	10	US-09-991-163-144	Sequence 144, App
C 831	14.8	0.6	42	10	US-09-780-662A-23	Sequence 23, App1	904	14.8	0.6	50	10	US-09-993-604-144	Sequence 144, App
C 832	14.8	0.6	42	10	US-09-873-737A-8	Sequence 8, App1	905	14.8	0.6	50	10	US-09-990-456-144	Sequence 144, App
C 833	14.8	0.6	42	10	US-09-954-737-20	Sequence 20, App1	906	14.8	0.6	50	10	US-09-944-243-5	Sequence 5, App1
C 834	14.8	0.6	43	10	US-09-771-425-12	Sequence 12, App1	907	14.8	0.6	50	10	US-09-969-721-144	Sequence 144, App
C 835	14.8	0.6	43	10	US-09-771-425-13	Sequence 13, App1	908	14.8	0.6	50	10	US-09-909-088B-79	Sequence 79, App1
C 836	14.8	0.6	43	10	US-09-746-359A-50	Sequence 50, App1	909	14.8	0.6	50	12	US-10-014-326-5	Sequence 5, App1
C 837	14.8	0.6	43	10	US-09-825-561A-61	Sequence 61, App1	910	14.6	0.6	21	10	US-09-946-805-10	Sequence 10, App1
C 838	14.8	0.6	45	8	US-08-973-028-6	Sequence 6, App1	911	14.6	0.6	22	10	US-09-853-830-126	Sequence 126, App
C 839	14.8	0.6	45	9	US-09-925-664-73	Sequence 73, App1	912	14.6	0.6	22	10	US-09-969-373-2202	Sequence 2202, App
C 840	14.8	0.6	45	10	US-09-732-914-123	Sequence 123, App	913	14.6	0.6	22	10	US-09-969-373-2706	Sequence 2706, App
C 841	14.8	0.6	45	10	US-09-827-289-12	Sequence 12, App1	914	14.6	0.6	24	10	US-09-791-500-14	Sequence 14, App1
C 842	14.8	0.6	45	10	US-09-842-552-49	Sequence 49, App1	915	14.6	0.6	24	10	US-09-215-652-39	Sequence 39, App1
C 843	14.8	0.6	45	10	US-09-065-040-23	Sequence 23, App1	916	14.6	0.6	24	10	US-09-740-668A-79	Sequence 79, App1
C 844	14.8	0.6	45	10	US-09-969-192-42	Sequence 42, App1	917	14.6	0.6	24	10	US-09-995-542-17	Sequence 17, App1
C 845	14.8	0.6	45	12	US-10-002-278-14	Sequence 14, App1	918	14.6	0.6	24	10	US-09-969-373-1623	Sequence 1623, App
C 846	14.8	0.6	46	9	US-10-106-092-6	Sequence 6, App1	919	14.6	0.6	25	10	US-09-864-680-7	Sequence 7, App1
C 847	14.8	0.6	46	10	US-09-835-147-21	Sequence 21, App1	920	14.6	0.6	25	10	US-09-866-108-10839	Sequence 10839, A
C 848	14.8	0.6	46	10	US-09-848-164-67	Sequence 67, App1	921	14.6	0.6	25	10	US-09-866-108-10840	Sequence 10840, A
C 849	14.8	0.6	46	10	US-09-848-164-68	Sequence 68, App1	922	14.6	0.6	25	10	US-09-866-108-10841	Sequence 10841, A
C 850	14.8	0.6	46	10	US-09-9419-305-14	Sequence 14, App1	923	14.6	0.6	25	10	US-09-866-108-10842	Sequence 10842, A
C 851	14.8	0.6	46	10	US-09-905-291A-358	Sequence 358, App	924	14.6	0.6	25	10	US-09-866-108-10843	Sequence 10843, A
C 852	14.8	0.6	47	9	US-09-886-942-35	Sequence 35, App1	925	14.6	0.6	25	10	US-09-866-108-11912	Sequence 11912, A
C 853	14.8	0.6	47	10	US-09-817-014-19	Sequence 19, App1	926	14.6	0.6	25	10	US-09-866-108-11913	Sequence 11913, A
C 854	14.8	0.6	47	10	US-09-901-484A-286	Sequence 286, App	927	14.6	0.6	25	10	US-09-866-108-11914	Sequence 11914, A
C 855	14.8	0.6	47	10	US-09-901-484A-334	Sequence 334, App	928	14.6	0.6	25	10	US-09-866-108-11915	Sequence 11915, A
C 856	14.8	0.6	47	10	US-09-909-320-358	Sequence 358, App	929	14.6	0.6	25	10	US-09-866-108-11916	Sequence 11916, A
C 857	14.8	0.6	47	10	US-09-909-088B-358	Sequence 358, App	930	14.6	0.6	25	10	US-09-866-108-13343	Sequence 13343, A
C 858	14.8	0.6	47	10	US-09-263-959-138	Sequence 138, App	931	14.6	0.6	25	10	US-09-866-108-13344	Sequence 13344, A
C 859	14.8	0.6	47	10	US-09-790-399-23	Sequence 23, App1	932	14.6	0.6	25	10	US-09-866-108-13345	Sequence 13345, A
C 860	14.8	0.6	48	9	US-09-944-413-119	Sequence 119, App	933	14.6	0.6	25	10	US-09-866-108-13346	Sequence 13346, A
C 861	14.8	0.6	48	10	US-09-866-028-119	Sequence 119, App	934	14.6	0.6	25	10	US-09-866-108-13347	Sequence 13347, A
C 862	14.8	0.6	48	10	US-09-944-449-119	Sequence 119, App	935	14.6	0.6	25	10	US-09-866-108-15403	Sequence 15403, A
C 863	14.8	0.6	48	10	US-09-944-457-119	Sequence 119, App	936	14.6	0.6	25	10	US-09-866-108-15404	Sequence 15404, A
C 864	14.8	0.6	48	10	US-09-916-940-74	Sequence 74, App1	937	14.6	0.6	25	10	US-09-750-373-49	Sequence 49, App1
C 865	14.8	0.6	48	10	US-09-945-587-119	Sequence 119, App	938	14.6	0.6	26	10	US-09-910-428-2	Sequence 2, App1
C 866	14.8	0.6	48	10	US-09-945-015-119	Sequence 119, App	939	14.6	0.6	27	10	US-09-949-713-7	Sequence 7, App1
C 867	14.8	0.6	48	10	US-09-944-396-119	Sequence 119, App	940	14.6	0.6	28	10	US-09-887-607-15	Sequence 15, App1
C 868	14.8	0.6	48	10	US-09-944-097-119	Sequence 119, App	941	14.6	0.6	28	10	US-09-834-666A-47	Sequence 47, App1
C 869	14.8	0.6	48	10	US-09-944-432-119	Sequence 119, App	942	14.6	0.6	29	9	US-09-863-040-49	Sequence 49, App1
C 870	14.8	0.6	48	10	US-09-943-762-119	Sequence 119, App	943	14.6	0.6	29	10	US-09-836-607-13	Sequence 13, App1
C 871	14.8	0.6	48	10	US-09-943-654-119	Sequence 119, App	944	14.6	0.6	29	10	US-09-836-607-15	Sequence 15, App1
C 872	14.8	0.6	48	10	US-09-918-601-74	Sequence 74, App1	945	14.6	0.6	29	10	US-09-940-037A-21	Sequence 21, App1
C 873	14.8	0.6	48	10	US-09-943-851A-119	Sequence 119, App	947	14.6	0.6	29	10	US-09-887-469-7	Sequence 7, App1
C 874	14.8	0.6	49	9	US-09-905-291A-8	Sequence 8, App1	948	14.6	0.6	29	12	US-10-040-916-58	Sequence 58, App1
C 875	14.8	0.6	49	10	US-09-740-002-10	Sequence 10, App1	949	14.6	0.6	30	8	US-08-834-666A-44	Sequence 44, App1
C 876	14.8	0.6	49	10	US-09-056-160B-43	Sequence 43, App1	950	14.6	0.6	30	9	US-09-840-242B-5	Sequence 5, App1
C 877	14.8	0.6	49	10	US-09-922-958-6	Sequence 6, App1	951	14.6	0.6	30	9	US-09-879-813-6	Sequence 6, App1
C 878	14.8	0.6	49	10	US-09-909-320-8	Sequence 8, App1	952	14.6	0.6	30	9	US-09-966-955A-10	Sequence 10, App1
C 879	14.8	0.6	49	10	US-09-909-088B-8	Sequence 8, App1	953	14.6	0.6	30	10	US-09-426-548-143	Sequence 143, App
C 880	14.8	0.6	49	12	US-10-090-624-25	Sequence 25, App1	954	14.6	0.6	30	10	US-09-797-518A-43	Sequence 43, App1
C 881	14.8	0.6	49	9	US-09-905-291A-79	Sequence 79, App1	955	14.6	0.6	30	10	US-09-231-235-43	Sequence 43, App1
C 882	14.8	0.6	50	9	US-09-992-598-144	Sequence 144, App	956	14.6	0.6	30	10	US-09-962-035-39	Sequence 39, App1
C 883	14.8	0.6	50	9	US-09-504-231A-2930	Sequence 2930, App	957	14.6	0.6	30	10	US-09-829-855-148	Sequence 148, App
C 884	14.8	0.6	50	10	US-09-504-231A-2930	Sequence 2930, App	958	14.6	0.6	30	10	US-09-797-518A-43	Sequence 43, App1
C 885	14.8	0.6	50	10	US-09-967-013-15	Sequence 15, App1	959	14.6	0.6	30	10	US-09-797-518A-43	Sequence 43, App1
C 886	14.8	0.6	50	10	US-09-967-013-16	Sequence 16, App1	960	14.6	0.6	30	10	US-09-333-557-17	Sequence 17, App1
C 887	14.8	0.6	50	10	US-09-869-722-144	Sequence 144, App	961	14.6	0.6	30	10	US-09-804-682-83	Sequence 83, App1
C 888	14.8	0.6	50	10	US-09-869-722-144	Sequence 144, App	962	14.6	0.6	30	10	US-09-753-352-47	Sequence 47, App1
C 889	14.8	0.6	50	10	US-09-989-273-144	Sequence 144, App	963	14.6	0.6	30	10	US-09-948-419A-39	Sequence 39, App1
C 890	14.8	0.6	50	10	US-09-989-273-144	Sequence 144, App	964	14.6	0.6	30	12	US-10-023-529-39	Sequence 39, App1
C 891	14.8	0.6	50	10	US-09-989-273-144	Sequence 144, App	965	14.6	0.6	30	12	US-10-013-030A-82	Sequence 82, App1
C 892	14.8	0.6	50	10	US-09-274-553D-2930	Sequence 2930, App	966	14.6	0.6	30	12	US-10-023-523-39	Sequence 39, App1
C 893	14.8	0.6	50	10	US-09-274-553D-2930	Sequence 2930, App	967	14.6	0.6	31	9	US-09-886-156-25	Sequence 25, App1
C 894	14.8	0.6	50	10	US-09-734-836-5	Sequence 5, App1	968	14.6	0.6	31	9	US-09-886-156-25	Sequence 25, App1

969 14.6 0.6 31 10 US-09-799-463-9 Sequence 9, Appli  
970 14.6 0.6 31 10 US-09-799-994-9 Sequence 9, Appli  
971 14.6 0.6 31 10 US-09-801-274-331 Sequence 331, App  
972 14.6 0.6 31 10 US-09-801-274-650 Sequence 650, App  
973 14.6 0.6 31 10 US-09-801-274-687 Sequence 687, App  
974 14.6 0.6 31 10 US-09-801-274-741 Sequence 741, App  
975 14.6 0.6 31 10 US-09-801-274-773 Sequence 773, App  
976 14.6 0.6 31 10 US-09-801-274-1230 Sequence 1230, Ap  
977 14.6 0.6 31 10 US-09-801-274-1358 Sequence 1358, Ap  
978 14.6 0.6 31 10 US-09-801-274-1452 Sequence 1452, Ap  
979 14.6 0.6 31 10 US-09-801-274-1530 Sequence 1530, Ap  
980 14.6 0.6 31 10 US-09-801-274-1599 Sequence 1599, Ap  
981 14.6 0.6 31 10 US-09-801-274-1621 Sequence 1621, Ap  
982 14.6 0.6 31 10 US-09-801-274-1723 Sequence 1723, Ap  
983 14.6 0.6 31 10 US-09-801-274-1776 Sequence 1776, Ap  
984 14.6 0.6 31 10 US-09-933-497B-4 Sequence 4, Appli  
985 14.6 0.6 32 10 US-09-765-272-374 Sequence 374, App  
986 14.6 0.6 32 10 US-09-759-667A-5 Sequence 5, Appli  
987 14.6 0.6 32 10 US-09-990-080-7 Sequence 7, Appli  
988 14.6 0.6 33 10 US-09-880-006-6 Sequence 6, Appli  
989 14.6 0.6 33 10 US-09-759-143-488 Sequence 488, App  
990 14.6 0.6 33 10 US-09-780-669-488 Sequence 488, App  
991 14.6 0.6 33 10 US-09-950-255-2 Sequence 2, Appli  
992 14.6 0.6 33 10 US-09-822-827-488 Sequence 488, App  
993 14.6 0.6 33 10 US-09-801-368-20 Sequence 20, Appli  
994 14.6 0.6 34 10 US-09-826-212-23 Sequence 23, Appli  
995 14.6 0.6 34 10 US-09-784-990-20 Sequence 20, Appli  
996 14.6 0.6 34 10 US-09-765-272-321 Sequence 321, App  
997 14.6 0.6 35 9 US-09-773-599-13 Sequence 13, Appli  
998 14.6 0.6 35 10 US-09-727-311-22 Sequence 22, Appli  
999 14.6 0.6 35 10 US-09-746-801A-68 Sequence 68, Appli  
1000 14.6 0.6 37 10 US-09-850-799-12 Sequence 12, Appli

## ALIGNMENTS

RESULT 1  
US-10-108-280-6  
; Sequence 6, Application US/10108280  
; Patent No. US20020115098A1  
; GENERAL INFORMATION:  
; APPLICANT: Sosnowski, Ronald G.  
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH  
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229  
; CURRENT APPLICATION NUMBER: US/10/108,280  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US/09/645,757  
; PRIOR FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin  
US-10-108-280-6

Query Match 1.0%; Score 22.8; DB 12; Length 49;  
Best Local Similarity 79.4%; Pred. No. 1e+04;  
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1978 CTCACATTTATCATTCATTCATTTATTCATT 2011  
Db 16 CTCATTCATTCATTCATTCATTCATTCATTCATT 49

RESULT 2  
US-09-975-408-59/c  
; Sequence 59, Application US/09975408  
; Patent No. US20020150917A1

; GENERAL INFORMATION:  
; APPLICANT: Nanogen, Inc.  
; APPLICANT: Weidenhammer, Elaine M.  
; APPLICANT: Xu, Xiao  
; APPLICANT: Kahl, Brenda F.  
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC  
; FILE REFERENCE: 267/174 Patrick S. Bagleman  
; CURRENT APPLICATION NUMBER: US/09/975,408  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 09/710,200  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 59  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Biotinylated  
US-09-975-408-59

Query Match 0.9%; Score 21.8; DB 10; Length 49;  
Best Local Similarity 70.7%; Pred. No. 1.8e+04;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1979 TCACATTTATCATTCATTCATTCATTTATTCATTGGGTTGTC 2019  
Db 46 TCATTCATTCATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 3  
US-10-075-579-59/c  
; Sequence 59, Application US/10075579  
; Patent No. US20020119484A1  
; GENERAL INFORMATION:  
; APPLICANT: Nanogen, Inc.  
; APPLICANT: Weidenhammer, Elaine M.  
; APPLICANT: Wang, Ling  
; APPLICANT: Xu, Xiao  
; APPLICANT: Heller, Michael J.  
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC  
; FILE REFERENCE: 256/262 Patrick S. Bagleman  
; CURRENT APPLICATION NUMBER: US/10/075,579  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/710,200  
; PRIOR FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 59  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Biotinylated  
US-10-075-579-59

Query Match 0.9%; Score 21.8; DB 12; Length 49;  
Best Local Similarity 70.7%; Pred. No. 1.8e+04;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1979 TCACATTTATCATTCATTCATTCATTTATTCATTGGGTTGTC 2019  
Db 46 TCATTCATTCATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 4  
US-09-920-171-27/c  
; Sequence 27, Application US/09920171



ADDRESS: Campbell and Flores



STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,851  
FILING DATE: 31-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/556,627  
FILING DATE: 13-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-944-851-9  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 0.8%; Score 19.4; DB 10; Length 21;  
Best Local Similarity 95.2%; Pred. No. 4.4e+04;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 GATGCATCCAGCGCCGACTCG 640  
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DB 21 GATGCATCCAGCGCCGACTAG 1

RESULT 12  
US-09-774-021-17  
Sequence 17, Application US/09774021  
Patent No. US20020102556A1  
GENERAL INFORMATION:  
APPLICANT: Laken, Steven J.  
APPLICANT: Kinzler, Kenneth W.  
TITLE OF INVENTION: Genotyping by Mass Spectrometric Analysis of Short DNA  
TITLE OF INVENTION: Fragments  
FILE REFERENCE: 01107.73601  
CURRENT APPLICATION NUMBER: US/09/774,021  
CURRENT FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: 09/198,340  
PRIOR FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 17  
LENGTH: 43  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer for PCR  
US-09-774-021-17

Query Match 0.8%; Score 19.4; DB 10; Length 43;  
Best Local Similarity 70.3%; Pred. No. 6.3e+04;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2030 TGTATGTATAAACATCTGTTTGGCTTATGTGCA 2066

|||||  
DB 3 TTTATGTATAAATTAATCTCTGAGGATTAATTGCA 39

RESULT 13  
US-09-809-905-4/C  
Sequence 4, Application US/09809905  
Patent No. US20020001806A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Yuanhui  
APPLICANT: Sun, Yi  
APPLICANT: Wang, Kevin Ka-Wang  
TITLE OF INVENTION: CASPASE-3S SPLICING VARIANT  
FILE REFERENCE: U.S. Application A0000224  
CURRENT APPLICATION NUMBER: US/09/809,905  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/204,468  
PRIOR FILING DATE: 2000-05-16  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 4  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-809-905-4

Query Match 0.8%; Score 19.2; DB 10; Length 40;  
Best Local Similarity 75.0%; Pred. No. 6.8e+04;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 925 GCTCACCAGAACTCTGATGATATAGC 956  
|||||  
DB 40 GCTCACAAGAACTCTATTTTATCCTAAC 9

RESULT 14  
US-09-944-851-5/C  
Sequence 5, Application US/09944851  
Patent No. US20020102648A1  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: Mch3, A No. US20020102648A1 Apoptotic Protease,  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,851  
FILING DATE: 31-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/556,627  
FILING DATE: 13-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001

```
;
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 19 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-851-5

Query Match      0.8%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 CTCTTCGCTATTCCACGG 719
Db 19 CTCTTCGCTATTCCACGG 1

RESULT 15
US-09-884-260A-48
; Sequence 48, Application US/09884260A
; Patent No. US20020098570A1
; GENERAL INFORMATION:
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: MUSKELON (CUCUMIS MELO) HYDROPEROXIDE
; FILE REFERENCE: 06027.0002U2
; CURRENT APPLICATION NUMBER: US/09/884,260A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 09//,537,357
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20020098570A1e -
US-09-884-260A-48

Query Match      0.8%; Score 19; DB 10; Length 46;
Best Local Similarity 71.4%; Pred. No. 8.1e+04;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1386 TATTGAGTGTCATTGATGATTTTTCATTTGCTT 1420
Db 9 TAGTGATGTGTGATGATGATTTAGTCACTTAGCTT 43

RESULT 16
US-09-284-249-2/C
; Sequence 2, Application US/09284249
; Patent No. US20020155510A1
; GENERAL INFORMATION:
; APPLICANT: Canterbury Health Limited
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Dendritic cell-specific antibodies
; FILE REFERENCE: 24309 MRB
; CURRENT APPLICATION NUMBER: US/09/284,249
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: PCT/NZ97/000134
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: NZ 299537
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 36
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Made in lab
US-09-284-249-2

Query Match      0.8%; Score 18.6; DB 9; Length 36;
Best Local Similarity 72.7%; Pred. No. 9e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1775 AGATGAGTGAGCTGACAGACATATAGAGAAATAC 1807
Db 35 AGAAATACAGACGACGACAGACGTAAGTGAATTC 3

RESULT 17
US-09-867-262-13
; Sequence 13, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: Frey, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward primer 9511TOPF
US-09-867-262-13

Query Match      0.8%; Score 18.6; DB 10; Length 39;
Best Local Similarity 72.7%; Pred. No. 9.3e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1911 AGCAGAGAGACAGACAAATGATGTPAAGCC 1943
Db 6 AGGAGAGAGAAATTACATGACGAGCGCTTTAGCC 38

RESULT 18
US-09-885-551A-13
; Sequence 13, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DUAVAKHISHVILI, Tsotne
; APPLICANT: Frey, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
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;; TITLE OF INVENTION: DIRECTED EVOLUTION  
;; FILE REFERENCE: DIVER1460-14  
;; CURRENT APPLICATION NUMBER: US/09/885,551A  
;; CURRENT FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: US/09/535,754  
;; PRIOR FILING DATE: 2000-03-27  
;; PRIOR APPLICATION NUMBER: US/09/522,289  
;; PRIOR FILING DATE: 2000-03-09  
;; NUMBER OF SEQ ID NOS: 14  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 13  
;; LENGTH: 39  
;; TYPE: DNA  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Forward primer 9511topf  
US-09-885-551A-13

Query Match 0.8%; Score 18.6; DB 10; Length 39;  
Best Local Similarity 72.7%; Pred. No. 9.3e+04;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1911 AGCGAGAGAGACAGACAGATGATGATAGCC 1943  
Db 6 AGCGAGAGATACATGACGCGCTTTAGCC 38

RESULT 19  
US-10-087-426-13  
; Sequence 13, Application US/10087426  
; Patent No. US20020142394A1  
; GENERAL INFORMATION:  
; APPLICANT: DIVERSA CORPORATION  
; APPLICANT: SHORT: JAY M.  
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION  
; FILE REFERENCE: DIVER1460-23  
; CURRENT APPLICATION NUMBER: US/10/087,426  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/276,860  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/267,118  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 09/246,178  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: US 09/185,373  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: US 08/760,489  
; PRIOR FILING DATE: 1996-11-05  
; PRIOR APPLICATION NUMBER: US 60/008,311  
; PRIOR FILING DATE: 1995-11-07  
; PRIOR APPLICATION NUMBER: US 08/962,504  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: US 08/677,112  
; PRIOR FILING DATE: 1996-07-09  
; PRIOR APPLICATION NUMBER: US 08/651,568  
; PRIOR FILING DATE: 1996-05-22  
; PRIOR APPLICATION NUMBER: US 60/008,316  
; PRIOR FILING DATE: 1995-11-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Forward primer 9511topf  
US-10-087-426-13

Query Match 0.8%; Score 18.6; DB 12; Length 39;  
Best Local Similarity 72.7%; Pred. No. 9.3e+04;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1911 AGCGAGAGAGACAGACAGATGATGATAGCC 1943

Db 6 AGCGAGAGATACATGACGCGCTTTAGCC 38

RESULT 20  
US-10-108-280-4  
; Sequence 4, Application US/10108280  
; Patent No. US20020115098A1  
; GENERAL INFORMATION:  
; APPLICANT: Sosnowski, Ronald G.  
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH  
; FILE REFERENCE: POLYMORPHISMS IN DNA  
; PRIOR APPLICATION NUMBER: US/10/108,280  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US/09/645,757  
; PRIOR FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin  
US-10-108-280-4

Query Match 0.8%; Score 18.6; DB 12; Length 41;  
Best Local Similarity 84.0%; Pred. No. 9.5e+04;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1987 TTATCCATTCATCATTCATTCATTCATT 2011  
Db 17 TCATTCATTCATTCATTCATTCATT 41

RESULT 21  
US-09-997-956-3  
; Sequence 3, Application US/09997956  
; Patent No. US20020106714A1  
; GENERAL INFORMATION:  
; APPLICANT: Jallink, Kees  
; TITLE OF INVENTION: Membrane Molecule Indicator Compositions  
; FILE REFERENCE: P-NS 5045  
; CURRENT APPLICATION NUMBER: US/09/997,956  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/250,679  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/256,559  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 42  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-997-956-3

Query Match 0.8%; Score 18.6; DB 10; Length 42;  
Best Local Similarity 72.7%; Pred. No. 9.6e+04;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 26 CCTACCGCGGTGGAGACGATGCGATGATCAG 58  
Db 1 CCTCGGCGCGGTACCGATATCAGATGTTGAG 33

RESULT 22  
US-09-771-372-1  
; Sequence 1, Application US/09771372

```
; Patent No. US20020160361A1
; GENERAL INFORMATION:
; APPLICANT: LOEHLEIN, CHRISTINE
; APPLICANT: POLIART, DAN
; APPLICANT: SHAHER, THOMAS
; APPLICANT: STEPHENS, KATHY
; APPLICANT: TAN, YUPING
; APPLICANT: WONG, LINDA
; APPLICANT: MONFORTE, JOSEPH
; TITLE OF INVENTION: METHODS FOR ANALYSIS OF GENE EXPRESSION
; FILE REFERENCE: 14-004510US
; CURRENT APPLICATION NUMBER: US/09/771,372
; CURRENT FILING DATE: 2001-01-27
; PRIOR APPLICATION NUMBER: 60/179,006
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-771-372-1
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```
Query Match          0.8%; Score 18.4; DB 9; Length 46;
Best Local Similarity 69.4%; Pred. No. 1.1e+05;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1571 TAGATGATTAAGACAGACCAACGACGAGAGCTG 1606
      ||| ||||| ||| ||| ||| ||| ||| ||| |||
DB 10 TATGAGATTAACGATAGCGCAACCGCGAGAGATG 45
```

```
RESULT 23
US-09-440-829-14
; Sequence 14, Application US/09440829
; Patent No. US20020160360A1
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Munishkin, Alexander
; APPLICANT: Simonenko, Peter
; TITLE OF INVENTION: Long Oligonucleotide Arrays
; FILE REFERENCE: C10N015
; CURRENT APPLICATION NUMBER: US/09/440,829
; CURRENT FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe s62_2_50
US-09-440-829-14
```

```
Query Match          0.8%; Score 18.4; DB 9; Length 50;
Best Local Similarity 69.4%; Pred. No. 1.2e+05;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1012 ATTTTATGCTCTGTGAATATTCAGAAATTCCTCC 1047
      ||| ||||| ||| ||||| ||||| ||||| |||||
DB 1 ATTCTTGAAGATCTGGAACCTTTCAGATGATGCTCC 36
```

```
RESULT 24
US-09-734-836-5/c
; Sequence 5, Application US/09734836
; Patent No. US20020098475A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020098475A1artlis AG
; TITLE OF INVENTION: Bovine Immunodeficiency Virus (BIV) Based Vectors
; FILE REFERENCE: 4-30922A
```

```
; CURRENT APPLICATION NUMBER: US/09/734,836
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/464,460
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; NAME/KEY: primer bind
; LOCATION: (1)..(50)
US-09-734-836-5
```

```
Query Match          0.8%; Score 18.2; DB 10; Length 50;
Best Local Similarity 74.2%; Pred. No. 1.3e+05;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 2224 CTTGATTAATGACTGTTTCTGCTGCTAAT 2254
      ||| ||||| ||| ||||| ||| |||||
DB 50 CTTTATTAAGCGCTGTTGCTTAAGCATTAAT 20
```

```
RESULT 25
US-09-944-851-8
; Sequence 8, Application US/09944851
; Patent No. US20020102648A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,851
; FILING DATE: 31-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/556,627
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1813
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SOURCE DESCRIPTION: SEQ ID NO: 8:
US-09-944-851-8
```

Query Match 0.8%; Score 18; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 ATGGCAGATGATCAGGCG 61  
|||||  
DB 1 ATGGCAGATGATCAGGCG 18

RESULT 26  
US-09-944-851-11/c  
; Sequence 11, Application US/09944851  
; Patent No. US20020102648A1  
GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomasselli, Kevin  
TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,  
Nucleic Acids Encoding and Methods of Use

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,851  
FILING DATE: 31-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/556,627  
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 1813

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-944-851-11

Query Match 0.8%; Score 18; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 977 GCTGAGAGCAATGGGTC 994  
|||||  
DB 18 GCTGAGAGCAATGGGTC 1

RESULT 27  
US-09-944-851-10  
; Sequence 10, Application US/09944851  
; Patent No. US20020102648A1  
GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa

Litwack, Gerald  
Armstrong, Robert  
Tomasselli, Kevin  
TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,  
Nucleic Acids Encoding and Methods of Use

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,851  
FILING DATE: 31-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/556,627  
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 1813

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-944-851-10

Query Match 0.8%; Score 18; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 TCGGGGCCCATCATGAC 655  
|||||  
DB 4 TCGGGGCCCATCATGAC 21

RESULT 28  
US-09-263-959-743/c  
; Sequence 743, Application US/09263959  
; Patent No. US20020150891A1  
GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 743:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-743

Query Match
Best Local Similarity 70.6%; Score 18; DB 10; Length 37;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1985 ATTATCATTCATTCATTCATTCATTCGTTGT 2018
Db 36 ATTATTTATTTATTTATTTATTTATTTATTTAT 3

RESULT 29
US-09-263-959-801/C
; Sequence 801, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 801:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-801

Query Match
Best Local Similarity 0.8%; Score 18; DB 10; Length 37;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1985 ATTATCATTCATTCATTCATTCATTCGTTGT 2018
```

```

; APPLICATION NUMBER: US/09/784,990
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 743:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-801

Query Match
Best Local Similarity 0.8%; Score 18; DB 10; Length 37;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1985 ATTATCATTCATTCATTCATTCATTCGTTGT 2018
Db 36 ATTATTTATTTATTTATTTATTTATTTATTTAT 3

RESULT 30
US-09-784-990-33/C
; Sequence 33, Application US/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 33
; LENGTH: 31
; TYPE: DNA
; ORGANISM: avian encephalomyelitis virus
; US-09-784-990-33

Query Match
Best Local Similarity 0.8%; Score 17.8; DB 10; Length 31;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 612 ACCTGATGATGATGATGATGATGATGATG 640
Db 30 ACCTTAATGACGGCTTCATTCATTCGACGCG 2

RESULT 31
US-09-839-743-1
; Sequence 1, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doeberner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; US-09-839-743-1

Query Match
Best Local Similarity 0.8%; Score 17.8; DB 10; Length 36;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1984 AATTATCATTCATTCATTCATTCATTCGTTG 2012
Db 5 AATTAAATCATTCATTCATTCATTCATTCGTTG 33
```

RESULT 32  
US-10-081-281-11/c  
Sequence 11, Application US/10081281  
Patent No. US20020151707A1  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne  
Gross, Jane A.  
Sheppard, Paul  
TITLE OF INVENTION: Immune Mediators and Related Methods  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,281  
FILING DATE: 20-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,811A  
FILING DATE: 03-Mar-1999  
APPLICATION NUMBER: US 08/480,002  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/482,133  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/483,241  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 60/005,964  
FILING DATE: 27-OCT-1995  
APPLICATION NUMBER: US 08/657,581  
FILING DATE: 07-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 014058-005630US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-081-281-11  
Query Match 0.8%; Score 17.8; DB 12; Length 37;  
Best Local Similarity 67.6%; Pred. No. 1.4e+05;  
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...45  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-962-055-30  
Query Match 0.8%; Score 17.8; DB 10; Length 45;  
Best Local Similarity 62.2%; Pred. No. 1.6e+05;  
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 71 GAGCAGGGGTTGAGGATTCAGCAATGAAGATTTCAGTGATGCT 115  
DB 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 34  
US-10-023-529-30  
Sequence 30, Application US/10023529.  
Patent No. US20020129388A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-529-30

Query Match 0.8%; Score 17.8; DB 12; Length 45;  
Best Local Similarity 62.2%; Pred. No. 1.6e+05;  
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 GAGCAGGGGTTGAGATTCAGCAATGAGATTCAGTGATGCT 115  
11 111 1 1111 11111111 11111 1  
Db 1 GAAGAGGAAGAAGATGATGATGAGATGAGATGAGATGAGATGAT 45

RESULT 35  
US-10-023-523-30  
Sequence 30, Application US/10023523  
Patent No. US20020152485A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Robert S.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,523  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-523-30

Query Match 0.8%; Score 17.8; DB 12; Length 45;  
Best Local Similarity 62.2%; Pred. No. 1.6e+05;  
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 GAGCAGGGGTTGAGATTCAGCAATGAGATTCAGTGATGCT 115  
11 111 1 1111 11111111 11111 1  
Db 1 GAAGAGGAAGAAGATGATGATGAGATGAGATGAGATGAGATGAT 45

RESULT 36  
US-09-956-086-32  
Sequence 32, Application US/09956086  
Patent No. US20020155498A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT

WHITLOW, MARC  
LEE, LISHYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..48  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-956-086-32

Query Match 0.8%; Score 17.8; DB 9; Length 48;  
Best Local Similarity 62.2%; Pred. No. 1.6e+05;  
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 155 AAGAAGAAAGAAATGTCACCATCGATCCATCAAGACCCGG 199  
11 1111 11111 1111 11111111 11111 1  
Db 4 AACAGACCAACACTACTACCAACAGACCAACACTACTACCGG 48

RESULT 37  
US-09-956-087-32  
Sequence 32, Application US/09956087  
Patent No. US20020161201A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LISHYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:



100

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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-334-954A-49

Query Match
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 91 AGCAATGACATTCAGTCGATGC 114
Db 5 AGCTATGACATTCGTCGCTGC 28

RESULT 41
US-09-985-442-13/c
; Sequence 13, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Ac
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-985-442-13

Query Match
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 145 CCTCTTCAGTAAGAAGAAAAA 168
Db 36 CGTCTTCAAAAAGAAAAAAA 13

RESULT 42
US-09-935-727-40/c
; Sequence 40, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
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; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward TNF-gamma-alpha primer
US-09-935-727-40

Query Match
Best Local Similarity 71.9%; Pred. No. 1.6e+05;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1179 GATTAATTTCTCTTGTATGCTGTACTT 1210
Db 35 GATTAATTTCTCATTTGGGAACCTGTAGACTT 4

RESULT 43
US-09-983-580-13/c
; Sequence 13, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-983-580-13

Query Match
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 145 CCTCTTCAGTAAGAAGAAAAA 168
Db 36 CGTCTTCAAAAAGAAAAAAA 13

RESULT 44
US-09-834-291-18
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; Sequence 18, Application US/09834291  
; Patent No. US20020042064A1  
; GENERAL INFORMATION:  
; APPLICANT: Krammer, Peter  
; APPLICANT: Muller-Schilling, Martina  
; APPLICANT: Oren, Moshe  
; TITLE OF INVENTION: p53 Binding Areas  
; FILE REFERENCE: 4121-122  
; CURRENT APPLICATION NUMBER: US/09/834,291  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: PCT/DE99/03343  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: DE 198 47 779.1  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; US-09-834-291-18

Query Match 0.8%; Score 17.6; DB 10; Length 40;  
Best Local Similarity 71.9%; Pred. No. 1.6e+05;  
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 558 AAACCTTTAGAGAAACCAACTCTTC 589  
Db 1 AATTAACCTTTAGAGATGCCCAACTGTTTC 32

RESULT 45  
US-09-834-291-26  
; Sequence 26, Application US/09834291  
; Patent No. US20020042064A1  
; GENERAL INFORMATION:  
; APPLICANT: Krammer, Peter  
; APPLICANT: Muller-Schilling, Martina  
; APPLICANT: Oren, Moshe  
; TITLE OF INVENTION: p53 Binding Areas  
; FILE REFERENCE: 4121-122  
; CURRENT APPLICATION NUMBER: US/09/834,291  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: PCT/DE99/03343  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: DE 198 47 779.1  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; US-09-834-291-26

Query Match 0.8%; Score 17.6; DB 10; Length 40;  
Best Local Similarity 71.9%; Pred. No. 1.6e+05;  
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 558 AAACCTTTAGAGAAACCAACTCTTC 589  
Db 1 AATTAACCTTTAGAGATGCCCAACTGTTTC 32

RESULT 46  
US-09-238-351-29  
; Sequence 29, Application US/09238351  
; Patent No. US2002000643A1  
; GENERAL INFORMATION:  
; APPLICANT: Kayem, Jon Paiz  
; APPLICANT: Bandad, Cynthia  
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic  
; TITLE OF INVENTION: Detection

; FILE REFERENCE: A67643/RFT/RMS  
; CURRENT APPLICATION NUMBER: US/09/238,351  
; CURRENT FILING DATE: 1999-01-27  
; EARLIER APPLICATION NUMBER: 09/014,304  
; EARLIER FILING DATE: 1998-01-27  
; EARLIER APPLICATION NUMBER: 60/073,011  
; EARLIER FILING DATE: 1998-01-29  
; EARLIER APPLICATION NUMBER: 60/084,425  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: 60/084,509  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: 60/078,102  
; EARLIER FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; US-09-238-351-29

Query Match 0.8%; Score 17.6; DB 10; Length 41;  
Best Local Similarity 65.0%; Pred. No. 1.7e+05;  
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1179 GATTAATTTCTCTTGTATGTCGTACCTGTTAATAG 1218  
Db 1 GATTACTGTGATGTGTGTCATCTGTGCATGAGTAG 40

RESULT 47  
US-09-737-626A-3/C  
; Sequence 3, Application US/09737626A  
; Patent No. US20020144304A1  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Plaskinski, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. US20020144304A1 Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/09/737,626A  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 42  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(42)  
; OTHER INFORMATION: fully synthetic sequence  
; US-09-737-626A-3

Query Match 0.8%; Score 17.6; DB 10; Length 42;  
Best Local Similarity 65.0%; Pred. No. 1.7e+05;  
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 152 AGTAAGAAGAGAAATGTCACCATGATCCATCAGA 191  
Db 40 ATATGCAAAAGAAAGAAATGAGACTGTATATCAAAAAA 1

RESULT 48  
US-10-104-611-18/C  
; Sequence 18, Application US/10104611  
; Patent No. US20020160976A1  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.

Mathews, Michael B.  
Katze, Michael G.  
Witherell, Gary  
Watson, Julia C.  
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/104,611  
FILING DATE: 22-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-104-611-18  
Query Match 0.8%; Score 17.6; DB 9; Length 45;  
Best Local Similarity 65.0%; Pred. No. 1.7e+05;  
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 1137 TTATATGTTATTCATTGGTGACTGCTAACTTCTCTT 1176  
Db 43 TTTGATGTCACCTCAGTGAGTATATCTACCTCTTTT 4  
RESULT 49  
US-10-112-547-18/c  
Sequence 18, Application US/10112547  
Patent No. US2002016097A1  
GENERAL INFORMATION:  
APPLICANT: Miles, Vincent J.  
Mathews, Michael B.  
Katze, Michael G.  
Witherell, Gary  
Watson, Julia C.  
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/112,547  
FILING DATE: 28-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-112-547-18  
Query Match 0.8%; Score 17.6; DB 9; Length 45;  
Best Local Similarity 65.0%; Pred. No. 1.7e+05;  
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 1137 TTATATGTTATTCATTGGTGACTGCTAACTTCTCTT 1176  
Db 43 TTTGATGTCACCTCAGTGAGTATATCTACCTCTTTT 4

RESULT 50  
US-09-965-602-27/c  
Sequence 27, Application US/09965602  
Patent No. US20020103154A1  
GENERAL INFORMATION:  
APPLICANT: Dimster-Denk, Dago  
TITLE OF INVENTION: ESSENTIAL GENES IN YEAST AS TARGETS FOR ANTIUNGAL  
TITLE OF INVENTION: AGENTS,  
FILE REFERENCE: ACA-8  
CURRENT APPLICATION NUMBER: US/09/965,602  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/539,697  
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 27  
LENGTH: 45  
TYPE: DNA  
ORGANISM: primer  
US-09-965-602-27  
Query Match 0.8%; Score 17.6; DB 10; Length 45;  
Best Local Similarity 65.0%; Pred. No. 1.7e+05;  
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 2221 ATTCTGATAATGACTGTTTTTTCCTTAATAGTAAAC 2260  
Db 44 ATTCTGTAAGAGTCGATTTTCTTTTGCATTTAC 5

Search completed: November 11, 2002, 02:38:41  
Job time : 144 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 22:35:37 ; Search time 449 Seconds

(without alignments)  
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Title: US-09-659-860A-3

Perfect score: 2309

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 2166140

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
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21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.2	50	22	AA127799 Human SNP oligonuc
2	39	1.7	50	22	AA127796 Human SNP oligonuc
3	28	1.2	28	24	ABK67234 Human gene specific
4	27.4	1.2	29	22	AA27845 Mutagenic upper pr
5	27.4	1.2	29	22	AA27846 Mutagenic lower pr
6	27.4	1.2	29	22	AA27846 Upper primer for g
7	27.4	1.2	29	22	AA27846 Lower primer for g
8	27	1.2	27	24	ABN80828 Human caspase 7 PC
9	27	1.2	27	24	ABK67138 Human gene specific

10	26	1.1	26	24	ABN80826 Human caspase 7 fo
11	26	1.1	26	24	ABK67137 Human gene specific
12	26	1.1	26	24	ABK67233 Human gene specific
13	25.6	1.1	48	22	AA013077 Mammalia caspase-3
14	25	1.1	47	21	AA269485 Human map-related
15	24.4	1.1	42	20	AA25254 Caspase-3 PCR prim
16	23.2	1.0	48	18	AA178319 Cysteine protease
17	22.8	1.0	30	18	AA178319 Cysteine protease
18	22.8	1.0	41	18	AAV06633 Transcription enha
19	22	1.0	30	18	AA178319 Cysteine protease
20	22	1.0	50	22	AA130903 Human SNP oligonuc
21	22	1.0	50	22	AA176189 Human silent SNP c
22	21.8	0.9	37	18	AAV06634 Transcription enha
23	21.8	0.9	38	21	AA178319 Cysteine protease
24	21.8	0.9	46	18	AA178319 Cysteine protease
25	21.8	0.9	49	24	ABN17653 Streptococcus agal
26	21.6	0.9	45	18	AA178319 Cysteine protease
27	21.4	0.9	45	22	AA178319 Cysteine protease
28	21.4	0.9	48	22	AA178319 Cysteine protease
29	21.4	0.9	50	22	AA178319 Cysteine protease
30	21.2	0.9	47	22	AA178319 Cysteine protease
31	21.2	0.9	48	22	AA178319 Cysteine protease
32	21	0.9	21	18	AA178319 Cysteine protease
33	21	0.9	33	18	AA178319 Cysteine protease
34	21	0.9	45	18	AA178319 Cysteine protease
35	21	0.9	47	22	AA178319 Cysteine protease
36	21	0.9	50	22	AA178319 Cysteine protease
37	20.8	0.9	41	21	AA178319 Cysteine protease
38	20.8	0.9	41	24	AA178319 Cysteine protease
39	20.8	0.9	48	22	AA178319 Cysteine protease
40	20.8	0.9	48	24	ABN1922 Streptococcus agal
41	20.8	0.9	49	16	AA178319 Cysteine protease
42	20.8	0.9	50	22	AA178319 Cysteine protease
43	20.8	0.9	50	23	AA178319 Cysteine protease
44	20.6	0.9	35	24	ABK6581 Newcastle disease
45	20.6	0.9	35	24	ABK6581 Newcastle disease
46	20.6	0.9	47	21	AA267746 Human map-related
47	20.6	0.9	50	22	AA130421 Human SNP oligonuc
48	20.6	0.9	50	22	AA179057 Human silent SNP c
49	20.4	0.9	50	19	AAV68378 Human silent SNP c
50	20.4	0.9	50	22	AA174543 Human silent SNP c
51	20.4	0.9	50	22	AA174543 Human silent SNP c
52	20.4	0.9	50	22	AA174543 Human silent SNP c
53	20.2	0.9	45	24	ABN1771 Streptococcus agal
54	20.2	0.9	47	24	ABN17830 Streptococcus agal
55	20.2	0.9	48	24	ABN17830 Streptococcus agal
56	20.2	0.9	49	13	AA034098 Downstream sequenc
57	20.2	0.9	50	18	AA176878 Streptococcus agal
58	20.2	0.9	50	20	AA15985 Streptococcus agal
59	20.2	0.9	50	20	AA15985 Streptococcus agal
60	20.2	0.9	50	22	AA130902 Human SNP oligonuc
61	20.2	0.9	50	22	AA177621 Human silent SNP c
62	20.2	0.9	50	22	AA179059 Human silent SNP c
63	20.2	0.9	50	22	AA179059 Human silent SNP c
64	20.2	0.9	50	24	ABN17629 Streptococcus agal
65	20	0.9	50	24	ABN80827 Human caspase 7 re
66	20	0.9	20	24	ABN80842 Human caspase 7 ph
67	20	0.9	20	24	ABN80843 Human caspase 7 ph
68	20	0.9	20	24	ABN80844 Human caspase 7 ph
69	20	0.9	20	24	ABN80845 Human caspase 7 ph
70	20	0.9	20	24	ABN80846 Human caspase 7 ph
71	20	0.9	20	24	ABN80847 Human caspase 7 ph
72	20	0.9	20	24	ABN80848 Human caspase 7 ph
73	20	0.9	20	24	ABN80849 Human caspase 7 ph
74	20	0.9	20	24	ABN80850 Human caspase 7 ph
75	20	0.9	20	24	ABN80851 Human caspase 7 ph
76	20	0.9	20	24	ABN80852 Human caspase 7 ph
77	20	0.9	20	24	ABN80853 Human caspase 7 ph
78	20	0.9	20	24	ABN80854 Human caspase 7 ph
79	20	0.9	20	24	ABN80855 Human caspase 7 ph
80	20	0.9	20	24	ABN80856 Human caspase 7 ph
81	20	0.9	20	24	ABN80857 Human caspase 7 ph
82	20	0.9	20	24	ABN80858 Human caspase 7 ph

C 83	20	0.9	20	24	ABN80859	Human caspase 7 ph	156	19.6	0.8	33	18	AAV06635	Transcription enh
C 84	20	0.9	20	24	ABN80860	Human caspase 7 ph	C 157	19.6	0.8	36	22	AAD09368	Toxoplasma gondii
C 85	20	0.9	20	24	ABN80861	Human caspase 7 ph	C 158	19.6	0.8	37	20	AAV19805	PCR primer FL5602
C 86	20	0.9	20	24	ABN80862	Human caspase 7 ph	C 159	19.6	0.8	42	17	AAAT4401	Homology vector 56
C 87	20	0.9	20	24	ABN80863	Human caspase 7 ph	C 160	19.6	0.8	42	21	AAZ95551	Pseudomonas putida
C 88	20	0.9	20	24	ABN80864	Human caspase 7 ph	C 161	19.6	0.8	47	21	AAZ68994	Human map-related
C 89	20	0.9	20	24	ABN80865	Human caspase 7 ph	C 162	19.6	0.8	50	10	AAAN1970	Complementary sequ
C 90	20	0.9	20	24	ABN80866	Human caspase 7 ph	C 163	19.6	0.8	50	22	AAAL28562	Human SNP oligonuc
C 91	20	0.9	20	24	ABN80867	Human caspase 7 ph	C 164	19.6	0.8	50	22	AAAL1835	Human SNP oligonuc
C 92	20	0.9	20	24	ABN80868	Human caspase 7 ph	C 165	19.6	0.8	50	24	ABN1766	Streptococcus agal
C 93	20	0.9	20	24	ABN80869	Human caspase 7 ph	C 166	19.4	0.8	21	18	AAT66975	CHN-1 mutagenic PC
C 94	20	0.9	20	24	ABN80870	Human caspase 7 ph	C 167	19.4	0.8	38	23	ABK08549	Apoptotic protease
C 95	20	0.9	20	24	ABN80871	Human caspase 7 ph	C 168	19.4	0.8	41	19	AAV50525	Human C20 Zinzyme
C 96	20	0.9	20	24	ABN80872	Human caspase 7 ph	C 169	19.4	0.8	41	19	AAV50525	Brassica sp. polym
C 97	20	0.9	20	24	ABN80873	Human caspase 7 ph	C 170	19.4	0.8	41	24	ABK12122	Brassica polyomorph
C 98	20	0.9	20	24	ABN80874	Human caspase 7 ph	C 171	19.4	0.8	41	24	ABK12123	Human hrdRI oligon
C 99	20	0.9	20	24	ABN80875	Human caspase 7 ph	C 172	19.4	0.8	43	21	AAA60141	Human hrdRI oligon
C 100	20	0.9	20	24	ABN80876	Human caspase 7 ph	C 173	19.4	0.8	46	24	ABO73450	Human APC gene var
C 101	20	0.9	20	24	ABN80877	Human caspase 7 ph	C 174	19.4	0.8	47	21	AAZ65912	LacZ model system
C 102	20	0.9	20	24	ABN80878	Human caspase 7 ph	C 175	19.4	0.8	47	21	AAZ65912	Human map-related
C 103	20	0.9	20	24	ABN80879	Human caspase 7 ph	C 176	19.4	0.8	47	21	AAZ65912	Human map-related
C 104	20	0.9	20	24	ABN80880	Human caspase 7 ph	C 177	19.4	0.8	47	21	AAZ68315	Human map-related
C 105	20	0.9	20	24	ABN80881	Human caspase 7 ph	C 178	19.4	0.8	47	21	AAZ68315	RBP-7 biallelic ma
C 106	20	0.9	20	24	ABN80882	Human caspase 7 ph	C 179	19.4	0.8	50	22	AAI28695	Human SNP oligonuc
C 107	20	0.9	20	24	ABN80883	Human caspase 7 ph	C 180	19.4	0.8	50	22	AAI28695	Human SNP oligonuc
C 108	20	0.9	20	24	ABN80884	Human caspase 7 ph	C 181	19.2	0.8	24	24	AAI33536	Human TTP8 specifl
C 109	20	0.9	20	24	ABN80885	Human caspase 7 ph	C 182	19.2	0.8	35	12	AAQ11882	Human TTP8 specifl
C 110	20	0.9	20	24	ABN80886	Human caspase 7 ph	C 183	19.2	0.8	36	17	AAAT38491	Probe NR-2 to arg1
C 111	20	0.9	20	24	ABN80887	Human caspase 7 ph	C 184	19.2	0.8	36	21	AAAC38491	Primer p5 (HutGM-C
C 112	20	0.9	20	24	ABN80888	Human caspase 7 ph	C 185	19.2	0.8	38	21	AAAI1855	Human foetal gene
C 113	20	0.9	20	24	ABN80889	Human caspase 7 ph	C 186	19.2	0.8	38	24	AAI45763	Cancer cells detec
C 114	20	0.9	20	24	ABN80890	Human caspase 7 ph	C 187	19.2	0.8	41	21	ABK1740	PCR primer for hum
C 115	20	0.9	20	24	ABN80891	Human caspase 7 ph	C 188	19.2	0.8	42	21	AAAC4425	Human telomerase (
C 116	20	0.9	20	24	ABN80892	Human caspase 7 ph	C 189	19.2	0.8	42	21	AAAC4425	Murine factor V 3
C 117	20	0.9	20	24	ABN80893	Human caspase 7 ph	C 190	19.2	0.8	45	20	AAAX9901	SP6 promoter CS pr
C 118	20	0.9	20	24	ABN80894	Human caspase 7 ph	C 191	19.2	0.8	46	24	ABN1679	Streptococcus agal
C 119	20	0.9	20	24	ABN80895	Human caspase 7 ph	C 192	19.2	0.8	47	21	AAZ65862	Human map-related
C 120	20	0.9	20	24	ABN80896	Human caspase 7 ph	C 193	19.2	0.8	47	21	AAZ65862	Human map-related
C 121	20	0.9	20	24	ABN80897	Human caspase 7 ph	C 194	19.2	0.8	47	21	AAZ68281	RBS primer used in
C 122	20	0.9	20	24	ABN80898	Human caspase 7 ph	C 195	19.2	0.8	48	22	AAAT9317	Primer base sequen
C 123	20	0.9	20	24	ABN80899	Human caspase 7 ph	C 196	19.2	0.8	49	19	AAV1447	Nucleotide sequen
C 124	20	0.9	20	24	ABN80900	Human caspase 7 ph	C 197	19.2	0.8	49	21	AAV1447	Liposome membrane-
C 125	20	0.9	20	24	ABN80901	Human caspase 7 ph	C 198	19.2	0.8	50	22	AAAT98419	Human SNP oligonuc
C 126	20	0.9	20	24	ABN80902	Human caspase 7 ph	C 199	19.2	0.8	50	22	AAAT98419	Human SNP oligonuc
C 127	20	0.9	20	24	ABN80912	Human caspase 7 ph	C 200	19.2	0.8	50	22	AAI28332	Apoptotic protease
C 128	20	0.9	20	24	ABN80918	Human caspase 7 ph	C 201	19.2	0.8	50	22	AAI28332	Hydroxyproline-ric
C 129	20	0.9	20	24	AAI45271	Human caspase 7 ph	C 202	19.2	0.8	50	22	AAI28332	Human NCO Zinzyme
C 130	20	0.9	20	24	ABN92444	Human papillomavir	C 203	19.2	0.8	50	22	AAI1687	Human inflammatory
C 131	20	0.9	20	24	AAV57975	Murine PSTIP N-te	C 204	19.2	0.8	19	18	ABK16994	phoA-luc construct
C 132	20	0.9	20	24	AAO7292	PCR primer for PST	C 205	19.2	0.8	36	24	ABK16994	Neisseria meningit
C 133	20	0.9	20	24	ABN1580	Thrombomodulin pro	C 206	19.2	0.8	40	22	AAH91677	Primer N5 for nove
C 134	20	0.9	20	24	ABN1580	Streptococcus agal	C 207	19.2	0.8	44	20	AAH91677	PCR primer N5, use
C 135	20	0.9	20	24	ABN1592	Streptococcus agal	C 208	19.2	0.8	45	21	AAH91677	Newcastle disease
C 136	20	0.9	20	24	AAK35015	Leader oligonucleo	C 209	19.2	0.8	45	21	AAH91677	PCR primer ocr90 f
C 137	20	0.9	20	24	AAK35436	Oligonucleotide us	C 210	19.2	0.8	45	21	AAH91677	PCR primer for det
C 138	20	0.9	20	24	ABK96211	Respiratory syncyt	C 211	19.2	0.8	46	22	AAI5891	Muskmelon 9-HPL pa
C 139	20	0.9	20	24	ABK96211	Respiratory syncyt	C 212	19.2	0.8	46	22	AAI5891	Primer #18. Unide
C 140	20	0.9	20	24	ABN71605	Streptococcus agal	C 213	19.2	0.8	47	21	AAZ67432	Human map-related
C 141	20	0.9	20	24	ABN71943	Streptococcus agal	C 214	19.2	0.8	47	21	AAZ67432	Human map-related
C 142	20	0.9	20	24	AAI55722	Murine caspase-9 R	C 215	19.2	0.8	47	21	AAZ67432	Human map-related
C 143	20	0.9	20	24	AAI55722	COX-2 promoter Ets	C 216	19.2	0.8	47	21	AAZ67432	Human map-related
C 144	20	0.9	20	24	AAI55722	Mouse splice accep	C 217	19.2	0.8	47	21	AAZ67432	Human map-related
C 145	20	0.9	20	24	AAI55722	Primer RM384 for	C 218	19.2	0.8	47	21	AAZ67432	Human map-related
C 146	20	0.9	20	24	AAI55722	Ceramide affinity	C 219	19.2	0.8	47	21	AAZ67432	Human map-related
C 147	20	0.9	20	24	AAI55722	DE19736591 primer	C 220	19.2	0.8	47	21	AAZ67432	Human map-related
C 148	20	0.9	20	24	AAI55722	PCR primer 3' Lac-S	C 221	19.2	0.8	47	21	AAZ67432	Human map-related
C 149	20	0.9	20	24	AAI55722	Streptococcus agal	C 222	19.2	0.8	47	21	AAZ67432	Human map-related
C 150	20	0.9	20	24	AAI55722	Primer for purmyc	C 223	19.2	0.8	48	20	AAH80033	PCR amplification
C 151	20	0.9	20	24	AAI55722	Human SNP oligonuc	C 224	19.2	0.8	49	20	AAH80033	B. thuringiensis c
C 152	20	0.9	20	24	AAI55722	Human SNP oligonuc	C 225	19.2	0.8	49	21	AAH80033	B. thuringiensis c
C 153	20	0.9	20	24	AAI55722	Human SNP oligonuc	C 226	19.2	0.8	49	21	AAH80033	B. thuringiensis c
C 154	20	0.9	20	24	AAI55722	Human SNP oligonuc	C 227	19.2	0.8	50	15	AAO74372	Capture probe Bb50
C 155	20	0.9	20	24	AAI55722	Human silent SNP c	C 228	19.2	0.8	50	22	AAI33808	Human SNP oligonuc

229	19	0.8	50	22	AA174720	Human silent SNP c
230	19	0.8	50	22	AA178577	Human silent SNP c
231	19	0.8	50	22	AA179055	Human silent SNP c
232	19	0.8	50	24	ABN71607	Streptococcus agal
233	18.8	0.8	37	20	AAAX91891	Porphyromonas ging
234	18.8	0.8	38	16	AAAT54160	Human ICAM hammerh
235	18.8	0.8	40	21	AAZ56316	Human peptidase NA
236	18.8	0.8	40	21	AAZ56317	Human peptidase NA
237	18.8	0.8	41	21	AAZ67718	Anti-human VEGF re
238	18.8	0.8	41	21	AAAF70195	Oligonucleotide SE
239	18.8	0.8	42	23	ABL54419	5' flanking region
240	18.8	0.8	42	23	ABL54421	#1 primer identifica
241	18.8	0.8	45	21	AAZ87717	Anti-human VEGF re
242	18.8	0.8	45	22	AAAF54940	PCR primer used to
243	18.8	0.8	45	22	AAAF70194	Oligonucleotide SE
244	18.8	0.8	45	22	AAAC82214	Human retrovirus D
245	18.8	0.8	46	18	AAAT65781	Repeat sequence fr
246	18.8	0.8	46	18	AAAT61263	Major outer membra
247	18.8	0.8	47	21	AAZ67480	Human map-related
248	18.8	0.8	47	21	AAZ67673	Human map-related
249	18.8	0.8	47	21	AAZ68365	CMS disorder-relat
250	18.8	0.8	47	23	AAH88353	Human leukocyte fu
251	18.8	0.8	48	18	AAO69476	Human LFA-1 gene T
252	18.8	0.8	48	18	AAAT63938	Test sequence from
253	18.8	0.8	48	20	AAAX17226	Primer base sequen
254	18.8	0.8	48	22	AAAF29310	Primer base sequen
255	18.8	0.8	48	22	AAAF29316	DNA binding molecu
256	18.8	0.8	48	24	ABK82717	Streptococcus agal
257	18.8	0.8	48	24	ABN71564	Primer Forward Lin
258	18.8	0.8	50	14	AAO37397	Primer MOVHLINK.
259	18.8	0.8	50	14	AAO37416	Trailer oligonucle
260	18.8	0.8	50	20	AAAX35021	PCR primer B1-7 us
261	18.8	0.8	50	20	AAAX15981	PCR primer B2-2 us
262	18.8	0.8	50	22	AAAX15984	Human SNP oligonuc
263	18.8	0.8	50	22	AAAL28051	Human SNP oligonuc
264	18.8	0.8	50	22	AAAL32299	Human SNP oligonuc
265	18.8	0.8	50	22	AAAL34092	Human SNP oligonuc
266	18.8	0.8	50	22	AAAT66209	Vector system rela
267	18.8	0.8	50	22	AAAT74543	Human silent SNP c
268	18.8	0.8	50	22	AAAT78431	Human silent SNP c
269	18.8	0.8	50	22	AAH89820	Human coding sequ
270	18.8	0.8	50	22	AAAF25442	Oligonucleotide us
271	18.8	0.8	50	24	ABK96217	Respiratory syncyt
272	18.8	0.8	50	24	ABK96217	Respiratory syncyt
273	18.8	0.8	50	24	ABK96217	Chimpanzee erythro
274	18.8	0.8	50	24	AAAC66888	Primer RMM389 for
275	18.8	0.8	50	24	AAAT14046	Humicola insolens
276	18.8	0.8	50	24	AAAT13428	PCR primer MK002 u
277	18.8	0.8	50	24	AAAT30252	Polynucleotide dir
278	18.8	0.8	50	24	AAAT60711	Forward PCR primer
279	18.8	0.8	50	24	AAAT97260	PCR primer 9511top
280	18.8	0.8	50	24	AAAT90020	Esterase gene 5' p
281	18.8	0.8	50	24	AAAT24098	Forward primer, 95
282	18.8	0.8	50	24	AAAT72842	Probe for B. thuri
283	18.8	0.8	50	24	AAAT27661	Probe used in clon
284	18.8	0.8	50	24	AAAD31620	Phosphatase 5 DNA p
285	18.8	0.8	50	24	AAAH48401	Human phospholipas
286	18.8	0.8	50	24	AAAB68895	FC-3 common probe
287	18.8	0.8	50	24	AAAS17877	Vaccinia virus pro
288	18.8	0.8	50	24	AAAB85475	Streptococcus agal
289	18.8	0.8	50	24	AAAB72388	Human map-related
290	18.8	0.8	50	24	AAAB68269	Human map-related
291	18.8	0.8	50	24	AAAL68923	Genotype assignmen
292	18.8	0.8	50	24	AAAL7414	Synthetic DNA temp
293	18.8	0.8	50	24	AAAL55276	Streptococcus agal
294	18.8	0.8	50	24	AAAB71565	Human interferon a
295	18.8	0.8	50	24	AAAB69717	Human interferon L
296	18.8	0.8	50	24	AAAB69719	Human interferon-a
297	18.8	0.8	50	24	AAAT64179	Human interferon L
298	18.8	0.8	50	24	AAAT64181	Test sequence from
299	18.8	0.8	50	24	AAAT17467	Test sequence from
300	18.8	0.8	50	24	AAAT17469	Human SNP oligonuc
301	18.8	0.8	50	24	AAAT28094	Human SNP oligonuc
302	18.8	0.8	50	24	AAAT28391	Human SNP oligonuc
303	18.8	0.8	50	24	AAAL31689	Human SNP oligonuc
304	18.8	0.8	50	24	AAAH90372	Human clone c94397
305	18.8	0.8	50	24	ABK82958	DNA binding molecu
306	18.8	0.8	50	24	ABK82960	DNA binding molecu
307	18.8	0.8	50	24	ABK82960	Streptococcus agal
308	18.8	0.8	50	24	ABN71844	Mouse caspase 7 ph
309	18.8	0.8	50	24	ABN80928	Mouse caspase 7 ph
310	18.8	0.8	50	24	ABN80936	Mouse caspase 7 ph
311	18.8	0.8	50	24	ABN80939	Mouse caspase 7 ph
312	18.8	0.8	50	24	ABN80940	Mouse caspase 7 ph
313	18.8	0.8	50	24	ABN80941	Mouse caspase 7 ph
314	18.8	0.8	50	24	ABN80946	Mouse caspase 7 ph
315	18.8	0.8	50	24	ABN80959	Mouse caspase 7 ph
316	18.8	0.8	50	24	AAAT31579	3' PCR primer for
317	18.8	0.8	50	24	AAAT31579	Oligonucleotide fo
318	18.8	0.8	50	24	AAAT31579	Dynamic hybridizat
319	18.8	0.8	50	24	AAAT31579	Human SNP oligonuc
320	18.8	0.8	50	24	AAAT31579	Human hydrogen per
321	18.8	0.8	50	24	AAAT31579	Human zinc finger
322	18.8	0.8	50	24	AAAT31579	Human peroxidase 2
323	18.8	0.8	50	24	AAAT31579	Microsatellite rep
324	18.8	0.8	50	24	AAAT31579	Fat regulated gene
325	18.8	0.8	50	24	AAAT31579	Human ASTH polymo
326	18.8	0.8	50	24	AAAT31579	Streptococcus agal
327	18.8	0.8	50	24	AAAT31579	PCR primer #4 use
328	18.8	0.8	50	24	AAAT31579	Human map-related
329	18.8	0.8	50	24	AAAT31579	Human map-related
330	18.8	0.8	50	24	AAAT31579	Human map-related
331	18.8	0.8	50	24	AAAT31579	Human map-related
332	18.8	0.8	50	24	AAAT31579	Human map-related
333	18.8	0.8	50	24	AAAT31579	Human map-related
334	18.8	0.8	50	24	AAAT31579	Human map-related
335	18.8	0.8	50	24	AAAT31579	Human map-related
336	18.8	0.8	50	24	AAAT31579	Human map-related
337	18.8	0.8	50	24	AAAT31579	Human map-related
338	18.8	0.8	50	24	AAAT31579	Human map-related
339	18.8	0.8	50	24	AAAT31579	Human map-related
340	18.8	0.8	50	24	AAAT31579	Human map-related
341	18.8	0.8	50	24	AAAT31579	Human map-related
342	18.8	0.8	50	24	AAAT31579	Human map-related
343	18.8	0.8	50	24	AAAT31579	Human map-related
344	18.8	0.8	50	24	AAAT31579	Human map-related
345	18.8	0.8	50	24	AAAT31579	Human map-related
346	18.8	0.8	50	24	AAAT31579	Human map-related
347	18.8	0.8	50	24	AAAT31579	Human map-related
348	18.8	0.8	50	24	AAAT31579	Human map-related
349	18.8	0.8	50	24	AAAT31579	Human map-related
350	18.8	0.8	50	24	AAAT31579	Human map-related
351	18.8	0.8	50	24	AAAT31579	Human map-related
352	18.8	0.8	50	24	AAAT31579	Human map-related
353	18.8	0.8	50	24	AAAT31579	Human map-related
354	18.8	0.8	50	24	AAAT31579	Human map-related
355	18.8	0.8	50	24	AAAT31579	Human map-related
356	18.8	0.8	50	24	AAAT31579	Human map-related
357	18.8	0.8	50	24	AAAT31579	Human map-related
358	18.8	0.8	50	24	AAAT31579	Human map-related
359	18.8	0.8	50	24	AAAT31579	Human map-related
360	18.8	0.8	50	24	AAAT31579	Human map-related
361	18.8	0.8	50	24	AAAT31579	Human map-related
362	18.8	0.8	50	24	AAAT31579	Human map-related
363	18.8	0.8	50	24	AAAT31579	Human map-related
364	18.8	0.8	50	24	AAAT31579	Human map-related
365	18.8	0.8	50	24	AAAT31579	Human map-related
366	18.8	0.8	50	24	AAAT31579	Human map-related
367	18.8	0.8	50	24	AAAT31579	Human map-related
368	18.8	0.8	50	24	AAAT31579	Human map-related
369	18.8	0.8	50	24	AAAT31579	Human map-related
370	18.8	0.8	50	24	AAAT31579	Human map-related
371	18.8	0.8	50	24	AAAT31579	Human map-related
372	18.8	0.8	50	24	AAAT31579	Human map-related
373	18.8	0.8	50	24	AAAT31579	Human map-related
374	18.8	0.8	50	24	AAAT31579	Human map-related

C 375	18.2	0.8	43	22	AAH43584	CHL primer, CHL3.	C 448	18	0.8	49	18	AAT80517	Hepatoma AS-30D Ty
C 376	18.2	0.8	43	22	AAA89306	Arabidopsis cystat	C 449	18	0.8	49	21	AAA37520	Yeast acyltransfer
C 377	18.2	0.8	44	22	AAO88920	Escherichia coli D	C 450	18	0.8	49	21	AAA07416	PCR primer B for G
C 378	18.2	0.8	45	22	AAAF8490	Chlamydia pneumonia	C 451	18	0.8	50	14	AAO46276	NF-1 gene exon 4 3
C 379	18.2	0.8	45	22	AAH47672	Nucleotide sequenc	C 452	18	0.8	50	19	AAV98668	Human EGF-R hairpi
C 380	18.2	0.8	45	24	ABLA9540	scFv antibody and	C 453	18	0.8	50	20	AAV52188	Synthetic plasmid
C 381	18.2	0.8	47	21	AAZ66570	Human map-related	C 454	18	0.8	50	22	AAAL28201	Human SNP oligonuc
C 382	18.2	0.8	47	21	AAZ66500	Human map-related	C 455	18	0.8	50	22	AAAL28226	Human SNP oligonuc
C 383	18.2	0.8	47	21	AAZ65037	Human map-related	C 456	18	0.8	50	22	AAAL28659	Human SNP oligonuc
C 384	18.2	0.8	47	21	AAZ69040	J65 used in const	C 457	18	0.8	50	22	AAAL31007	Human SNP oligonuc
C 385	18.2	0.8	48	18	AAT74743	S. cerevisiae CDC2	C 458	18	0.8	50	22	AAAL31672	Human SNP oligonuc
C 386	18.2	0.8	48	20	AAAX78649	Human EGF-R hairpi	C 459	18	0.8	50	22	AAAL34137	Human SNP oligonuc
C 387	18.2	0.8	48	24	AAAS98511	Human protective D	C 460	18	0.8	50	22	AAAT73441	Human SNP oligonuc
C 388	18.2	0.8	50	19	AAV98920	Potato citrate syn	C 461	18	0.8	50	22	AAAT73653	Human silent SNP c
C 389	18.2	0.8	50	19	AAV98194	Human SNP oligonuc	C 462	18	0.8	50	22	AAAT75304	Human silent SNP c
C 390	18.2	0.8	50	22	AAAL29227	Human SNP oligonuc	C 463	18	0.8	50	22	AAAH20255	Human silent SNP c
C 391	18.2	0.8	50	22	AAAL29227	Human SNP oligonuc	C 464	18	0.8	50	24	ABN71966	PCR primer Vhr3 f
C 392	18.2	0.8	50	22	AAAL31223	Human SNP oligonuc	C 465	18	0.8	50	24	AAAS20798	Streptococcus agal
C 393	18.2	0.8	50	22	AAAL31731	Human SNP oligonuc	C 466	17.8	0.8	30	20	AAAZ10924	Clostridium diflic
C 394	18.2	0.8	50	22	AAAL34052	Human SNP oligonuc	C 467	17.8	0.8	30	24	AAAO1217	Primer for soluble
C 395	18.2	0.8	50	22	AAAT75302	Human silent SNP c	C 468	17.8	0.8	31	19	AAV93837	PCR primer #3. Sy
C 396	18.2	0.8	50	22	AAAT76998	Human clone c94332	C 469	17.8	0.8	33	16	AAAT05786	CD8-alpha hinge pc
C 397	18.2	0.8	50	22	AAAH90588	Human silent SNP c	C 470	17.8	0.8	33	22	AAAH28309	3' untranslated re
C 398	18.2	0.8	50	22	AAAH26139	Primer BHAS contai	C 471	17.8	0.8	33	24	ABAA4213	Human p80-colline
C 399	18.2	0.8	50	22	ABN71748	Human DNA containi	C 472	17.8	0.8	35	18	AAAT93837	Phosphodiester ol1
C 400	18.2	0.8	50	22	AAAT6997	Streptococcus agal	C 473	17.8	0.8	36	19	AAV09780	Tobacco PABF probe
C 401	18	0.8	18	18	AAAT6997	Apoptotic protease	C 474	17.8	0.8	37	18	AAAT47129	Primer for alpha c
C 402	18	0.8	18	18	AAAT67000	Apoptotic protease	C 475	17.8	0.8	37	22	AAAF31524	Oligonucleotide #2
C 403	18	0.8	24	18	AAAT66999	A thaliana GAD2 co	C 476	17.8	0.8	38	12	AAO10700	Mutagenising oligo
C 404	18	0.8	32	24	AAAL3424	Viral chemokine VM	C 477	17.8	0.8	38	12	AAAT82036	Human c-myp hamme
C 405	18	0.8	34	24	AAAD36347	PCR primer CHVP95	C 478	17.8	0.8	38	24	ABK20900	Human ENG C-cleave
C 406	18	0.8	34	24	AAAD36347	Fragment of cDNA e	C 479	17.8	0.8	39	13	AAO25328	3mer-A probe to F
C 407	18	0.8	35	16	AAAT01467	Inttron-exon juncti	C 480	17.8	0.8	39	16	AAAT51518	Fragment of cDNA e
C 408	18	0.8	36	16	AAAT01497	Truncated ssDNA 11	C 481	17.8	0.8	39	19	AAV30891	Human p53UBC hybr
C 409	18	0.8	36	16	AAO85389	Human p53UBC hybr	C 482	17.8	0.8	39	19	AAV23335	Human Factor-VIII
C 410	18	0.8	36	16	AAO85389	Urease gene PCR pr	C 483	17.8	0.8	40	24	AAAC89275	Human brain T calic
C 411	18	0.8	36	19	AAV43366	Helicobacter ureb	C 484	17.8	0.8	41	24	AAAL36943	ECORT linker prime
C 412	18	0.8	36	19	AAV43366	Human NCO Zinzyme	C 485	17.8	0.8	41	24	AAAL36943	Human large protei
C 413	18	0.8	38	16	AAO75324	Maize polymorphic	C 486	17.8	0.8	42	19	AAV30729	Ubch5 protein 11.4
C 414	18	0.8	38	16	AAO75324	Primer specific to	C 487	17.8	0.8	42	24	ABK87864	Telomerase reverse
C 415	18	0.8	38	17	AAAT5685	Human ribosomal s7	C 488	17.8	0.8	42	24	ABK87864	Mouse MHC OVA PCR
C 416	18	0.8	38	23	ABK05765	Human NCO Zinzyme	C 489	17.8	0.8	42	24	AAAT61828	Mouse MHC OVA PCR
C 417	18	0.8	41	19	AAZ48936	Human NCO Zinzyme	C 490	17.8	0.8	44	18	AAAT61828	Heat shock protein
C 418	18	0.8	41	21	AAZ48936	Primer specific to	C 491	17.8	0.8	44	18	AAAT61828	Heat shock protein
C 419	18	0.8	41	21	ABAO2969	Human ribosomal s7	C 492	17.8	0.8	44	18	AAAT61828	CYP7B2 and CYP79B
C 420	18	0.8	42	20	ABN84399	CD8 alpha cDNA amp	C 493	17.8	0.8	45	15	AAO69442	Human interferon-a
C 421	18	0.8	43	20	AAAX81695	Tryptophan indole	C 494	17.8	0.8	45	20	AAAT28492	Human interferon-a
C 422	18	0.8	43	24	AAAL46476	Primer used in a n	C 495	17.8	0.8	45	20	AAAT28492	PCR primer SNS-Up.
C 423	18	0.8	43	24	ABAO4135	M catarrhalis MCAL	C 496	17.8	0.8	45	20	AAAT28492	Test sequence from
C 424	18	0.8	44	21	AAAT4331	Symbiodactylum to	C 497	17.8	0.8	45	20	AAAT28492	Primer for Ngop II
C 425	18	0.8	44	21	AAAT4331	Lobliolly pine SSR	C 498	17.8	0.8	45	20	AAAT28492	Low density lipopr
C 426	18	0.8	45	16	AAAT07603	RT-PCR primer/prob	C 499	17.8	0.8	45	22	AAH26502	DNA binding molecu
C 427	18	0.8	45	16	AAAT07602	RT-PCR primer/prob	C 500	17.8	0.8	46	22	ABK82683	Human map-related
C 428	18	0.8	45	16	AAO26268	Oligonucleotide #2	C 501	17.8	0.8	46	22	AAAL28897	Human map-related
C 429	18	0.8	46	21	AAAT71084	Oligonucleotide #1	C 502	17.8	0.8	47	15	AAO66785	Ribozyme substrate
C 430	18	0.8	46	21	AAAT71084	Molecular interact	C 503	17.8	0.8	47	21	AAZ65999	Human map-related
C 431	18	0.8	46	21	AAAT71085	Molecular interact	C 504	17.8	0.8	47	21	AAZ65999	Human map-related
C 432	18	0.8	46	21	AAAT71098	Molecular interact	C 505	17.8	0.8	47	21	AAZ65999	Human map-related
C 433	18	0.8	46	21	AAAT71102	Molecular interact	C 506	17.8	0.8	47	21	AAZ65999	Human map-related
C 434	18	0.8	46	21	AAAT71103	Molecular interact	C 507	17.8	0.8	47	21	AAZ65999	Human map-related
C 435	18	0.8	47	14	AAO38716	EBV detecting prim	C 508	17.8	0.8	47	21	AAZ65999	Human map-related
C 436	18	0.8	47	14	AAO38716	Oligonucleotide fo	C 509	17.8	0.8	47	21	AAZ65999	Human map-related
C 437	18	0.8	47	21	AAAT70139	Primer for human M	C 510	17.8	0.8	47	21	AAZ65999	Human map-related
C 438	18	0.8	47	21	AAZ66248	Human map-related	C 511	17.8	0.8	47	21	AAZ65999	Human map-related
C 439	18	0.8	47	21	AAZ66514	Human map-related	C 512	17.8	0.8	47	21	AAZ65999	Human map-related
C 440	18	0.8	47	21	AAZ66649	Human map-related	C 513	17.8	0.8	47	21	AAZ65999	Human map-related
C 441	18	0.8	47	21	AAZ67085	Human map-related	C 514	17.8	0.8	47	21	AAZ65999	Human map-related
C 442	18	0.8	47	21	AAZ67138	Human map-related	C 515	17.8	0.8	47	21	AAZ65999	Human map-related
C 443	18	0.8	47	21	AAZ67544	Human map-related	C 516	17.8	0.8	47	21	AAZ65999	Human map-related
C 444	18	0.8	47	21	AAZ68037	Human map-related	C 517	17.8	0.8	47	21	AAZ65999	Human map-related
C 445	18	0.8	47	21	AAZ68195	Human map-related	C 518	17.8	0.8	48	15	AAO69445	RBP-7 diallelic ma
C 446	18	0.8	47	21	AAZ68492	Human map-related	C 519	17.8	0.8	48	15	AAO69445	Human interferon-a
C 447	18	0.8	48	24	ABK11923	Human map-related	C 520	17.8	0.8	48	18	AAAT63907	Human map-related
C 448	18	0.8	48	24	ABK11923	Amino-RNA sequence	C 521	17.8	0.8	48	18	AAAT63907	Human map-related



C 521	17.8	0.8	48	20	AAK17195	Test sequence from
C 522	17.8	0.8	48	21	AAE89314	HPV 83 ori DNA fra
C 523	17.8	0.8	48	24	ABK82686	DNA binding molecu
C 524	17.8	0.8	48	24	ABN71541	Streptococcus agal
C 525	17.8	0.8	49	13	AAO24354	Oligonucleotide pri
C 526	17.8	0.8	49	19	AAV36530	Self-cleaving G8 D
C 527	17.8	0.8	49	24	ABN71750	Streptococcus agal
C 528	17.8	0.8	49	24	ABN71751	Streptococcus agal
C 529	17.8	0.8	49	24	ABN71987	Streptococcus agal
C 530	17.8	0.8	49	24	ABN72330	Streptococcus agal
C 531	17.8	0.8	50	20	AAK52058	Synthetic plasmid
C 532	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 533	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 534	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 535	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 536	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 537	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 538	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 539	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 540	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 541	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 542	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 543	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 544	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 545	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 546	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 547	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 550	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 556	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 558	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 559	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 563	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 564	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 565	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 566	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 567	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 571	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 573	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
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C 577	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 578	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 579	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 580	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 581	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 582	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 583	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 584	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 585	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 586	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 587	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 588	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 589	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 590	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 591	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 592	17.8	0.8	50	22	AAE28957	Human SNP oligonuc
C 593	17.8	0.8	50	22	AAE28957	Human SNP oligonuc

c 667	17.6	0.8	50	22	AAI32445	Human SNP oligonuc	c 740	17.4	0.8	47	24	ABN71571	Streptococcus agal
c 668	17.6	0.8	50	22	AAI34424	Human SNP oligonuc	c 741	17.4	0.8	47	24	ABN71626	Streptococcus agal
c 669	17.6	0.8	50	22	AAI34425	Human SNP oligonuc	c 742	17.4	0.8	47	24	ABN71665	Streptococcus agal
c 670	17.6	0.8	50	22	AAI34550	Human SNP oligonuc	c 743	17.4	0.8	47	24	ABN71710	Streptococcus agal
c 671	17.6	0.8	50	22	AAI34530	Human SNP oligonuc	c 744	17.4	0.8	47	24	ABN71908	Streptococcus agal
c 672	17.6	0.8	50	22	AAI76475	Cornedoesmosin sin	c 745	17.4	0.8	47	24	ABL76075	Streptococcus agal
c 673	17.6	0.8	50	22	AAI76599	Human silent SNP c	c 746	17.4	0.8	50	13	AAO35568	M. jannaschii com
c 674	17.6	0.8	50	22	AAI77311	Human silent SNP c	c 747	17.4	0.8	50	18	AAV76438	Linker pMSYN276
c 675	17.6	0.8	50	22	AAI77625	Human silent SNP c	c 748	17.4	0.8	50	19	AAV98891	Staphylococcus air
c 676	17.6	0.8	50	22	AAH89691	Human synthase cod	c 749	17.4	0.8	50	19	AAV98637	Human EGF-R hairpi
c 677	17.6	0.8	50	24	ABK82962	DNA binding molecu	c 750	17.4	0.8	50	19	AAV68981	Solanidine glucosy
c 678	17.6	0.8	50	24	ABN75034	Human SYCP1 +1 cM	c 751	17.4	0.8	50	21	AAAC80961	DNA molecule encod
c 679	17.6	0.8	50	24	ABN71608	Streptococcus agal	c 752	17.4	0.8	50	21	AAZ65176	Oligonucleotide ON
c 680	17.4	0.8	20	24	ABN80916	Human caspase 7 ph	c 753	17.4	0.8	50	22	AAI28200	Probe specific for
c 681	17.4	0.8	25	21	AAAC95929	HLA HLA-B gene PCR	c 754	17.4	0.8	50	22	AAI28550	Human SNP oligonuc
c 682	17.4	0.8	29	20	AAI29752	Oligo G11top for c	c 755	17.4	0.8	50	22	AAI28855	Human SNP oligonuc
c 683	17.4	0.8	29	22	AAI29752	Neisseria meningit	c 756	17.4	0.8	50	22	AAI28855	Human SNP oligonuc
c 684	17.4	0.8	29	22	AAI29752	Neisseria meningit	c 757	17.4	0.8	50	22	AAI28855	Human SNP oligonuc
c 685	17.4	0.8	29	22	AAI29752	Neisseria meningit	c 758	17.4	0.8	50	22	AAI28855	Human SNP oligonuc
c 686	17.4	0.8	30	18	AAI73408	N meningitidis fu	c 759	17.4	0.8	50	22	AAI30089	Human SNP oligonuc
c 687	17.4	0.8	30	20	AAI56441	Sl2 gene mutation	c 760	17.4	0.8	50	22	AAI31046	Human SNP oligonuc
c 688	17.4	0.8	30	20	AAI56441	Mouse VEGF PCR for	c 761	17.4	0.8	50	22	AAI31463	Human SNP oligonuc
c 689	17.4	0.8	30	20	AAI56441	Oncorhynchus nerka	c 762	17.4	0.8	50	22	AAI31463	Human SNP oligonuc
c 690	17.4	0.8	33	22	AAH75914	Bore-stimulatory p	c 763	17.4	0.8	50	22	AAI31463	Human SNP oligonuc
c 691	17.4	0.8	33	22	AAH75914	PCR primer #2 used	c 764	17.4	0.8	50	22	AAI31573	Human SNP oligonuc
c 692	17.4	0.8	35	22	AAI28195	PCR primer used to	c 765	17.4	0.8	50	22	AAI31573	Human SNP oligonuc
c 693	17.4	0.8	36	14	AAO48313	PCR primer for amp	c 766	17.4	0.8	50	22	AAI31573	Human SNP oligonuc
c 694	17.4	0.8	36	12	AAI28248	3' primer for huma	c 767	17.4	0.8	50	22	AAI77333	Cornedoesmosin sin
c 695	17.4	0.8	36	22	AAI28248	P. falciparum gcp	c 768	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 696	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 769	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 697	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 770	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 698	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 771	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	37	21	AAI28248	P. falciparum gcp	c 772	17.4	0.8	50	22	AAI77623	Human silent SNP c
c 699	17.4	0.8	3										

813	17.2	0.7	37	24	AA169499	M. utilissima S-hy	c 886	17.2	0.7	47	21	AAZ99608	3' PCR primer used
814	17.2	0.7	38	19	AAV85759	LTP5 exon primer 5	c 887	17.2	0.7	47	22	AAAL07489	Human reproductiv
815	17.2	0.7	38	19	AAV85837	LTP5 SNP primer 57	c 888	17.2	0.7	47	22	AAPE9150	Site-1 protease fu
816	17.2	0.7	38	23	ABK05814	Human MOG0 Zinyme	c 889	17.2	0.7	47	22	AAH20270	PCR primer VHP#3 f
817	17.2	0.7	38	24	ABK21079	Human ERG G-cleave	c 890	17.2	0.7	47	22	ABN71984	Streptococcus agal
818	17.2	0.7	39	12	AAQ11405	Probe COD 1359 spe	c 891	17.2	0.7	47	24	ABK40795	Human obesity-asso
819	17.2	0.7	39	19	AAV21263	Tissue plasminogen	c 892	17.2	0.7	48	21	AAAT14207	Beta-actin gene an
820	17.2	0.7	39	21	AAZ24220	M. thermophila lac	c 893	17.2	0.7	48	21	AAZ55690	HAEPV transfer vec
821	17.2	0.7	39	22	AAH43241	NIC primer #4. Sy	c 894	17.2	0.7	48	22	AAFP29298	primer base sequen
822	17.2	0.7	40	20	AAZ20807	Oligonucleotide en	c 895	17.2	0.7	48	22	AAFP29299	primer base sequen
823	17.2	0.7	40	20	AAZ76775	PCR primer for S.	c 896	17.2	0.7	48	22	AAFP29311	Primer base sequen
824	17.2	0.7	40	20	AAZ76776	Probe for Human DS	c 897	17.2	0.7	48	24	ABN71741	Streptococcus agal
825	17.2	0.7	40	20	AAZ01289	HSP75 sense primer	c 898	17.2	0.7	48	24	ABN71801	Streptococcus agal
826	17.2	0.7	40	21	AAZ94862	Primer 13A used to	c 899	17.2	0.7	49	20	AAZ19324	Streptococcus agal
827	17.2	0.7	40	21	AAZ61342	Signalling probe D	c 900	17.2	0.7	49	16	AAO85476	Vaccinia virus pro
828	17.2	0.7	40	21	AAZ40150	Signalling probe D	c 901	17.2	0.7	49	16	AAO88121	Stem-loop oligonuc
829	17.2	0.7	40	22	AAZ30176	Nucleoside deoxyri	c 902	17.2	0.7	49	17	AAAT72197	Stem loop oligonuc
830	17.2	0.7	40	24	ABL40580	Sequence of a muta	c 903	17.2	0.7	49	17	AAAT6592	Protein antigen b
831	17.2	0.7	41	13	AAO27446	Maize polymorphic	c 904	17.2	0.7	49	17	AAAT6517	PCR primer ZC6302.
832	17.2	0.7	41	19	AAV51085	Maize polymorphic	c 905	17.2	0.7	49	24	ABN71561	Streptococcus agal
833	17.2	0.7	41	19	AAV47833	Human neurofibroma	c 906	17.2	0.7	49	24	ABN71561	Streptococcus agal
834	17.2	0.7	41	24	ABK51379	Human neurofibroma	c 907	17.2	0.7	49	24	ABN71794	Intergenic region
835	17.2	0.7	41	24	ABK51380	Human ribosomal pr	c 908	17.2	0.7	50	12	AAQ11296	Analyte capture pr
836	17.2	0.7	41	24	ABA99834	Human RalBp1 assoc	c 909	17.2	0.7	50	12	AAQ12942	Analyte capture pr
837	17.2	0.7	41	24	AB199951	Human G protein 10	c 910	17.2	0.7	50	12	AAQ12941	Human MHC class II
838	17.2	0.7	41	24	ABL40240	Human phosphoribos	c 911	17.2	0.7	50	15	AAO69640	Human involucrin m
839	17.2	0.7	41	24	ABA02811	Human insulin-like	c 912	17.2	0.7	50	15	AAO69594	Human involucrin m
840	17.2	0.7	41	24	ABA02131	Human insulin-like	c 913	17.2	0.7	50	18	AAV76429	Staphylococcus aur
841	17.2	0.7	41	24	ABA02132	Oligonucleotide pr	c 914	17.2	0.7	50	18	AAV74392	HIV analyte captur
842	17.2	0.7	41	24	AAZ02082	PCR primer used to	c 915	17.2	0.7	50	18	AAV74391	Human involucrin m
843	17.2	0.7	42	21	AAZ59372	T. reesei xylanase	c 916	17.2	0.7	50	18	AAAT64056	Human MHC class II
844	17.2	0.7	42	21	AAA48228	T. reesei xylanase	c 917	17.2	0.7	50	18	AAAT64102	Human complement C
845	17.2	0.7	42	21	AAA48257	C. parvum Cp15/60 p	c 918	17.2	0.7	50	19	AAV71989	Synthetic plasmid
846	17.2	0.7	42	22	AAH45890	Artificial HaEPV D	c 919	17.2	0.7	50	20	AAZ52159	Synthetic plasmid
847	17.2	0.7	43	21	AAZ55693	Probe for Human im	c 920	17.2	0.7	50	20	AAZ52041	Test sequence from
848	17.2	0.7	43	22	AAZ55698	Artificial HaEPV D	c 921	17.2	0.7	50	20	AAZ52041	Test sequence from
849	17.2	0.7	44	21	AAZ55692	Tag DNA polymerase	c 922	17.2	0.7	50	20	AAZ52041	Test sequence from
850	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 923	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
851	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 924	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
852	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 925	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
853	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 926	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
854	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 927	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
855	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 928	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
856	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 929	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
857	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 930	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
858	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 931	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
859	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 932	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
860	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 933	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
861	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 934	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
862	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 935	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
863	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 936	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
864	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 937	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
865	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 938	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
866	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 939	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
867	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 940	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
868	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 941	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
869	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 942	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
870	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 943	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
871	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 944	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
872	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 945	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
873	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 946	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
874	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 947	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
875	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 948	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
876	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 949	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
877	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 950	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
878	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 951	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
879	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 952	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
880	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 953	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
881	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 954	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
882	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 955	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
883	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 956	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
884	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 957	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o
885	17.2	0.7	44	22	AAZ55692	Human oestrogen re	c 958	17.2	0.7	50	21	AAZ54011	E. coli K12 DNAs o

959	17	0.7	31	20	AAK38961	Human genomic DNA
960	17	0.7	32	18	AAK90574	Primer for CAEV im
961	17	0.7	33	24	ABK11844	Human dihydroxyrim
962	17	0.7	34	16	AAK02524	peni gene downstre
963	17	0.7	34	18	AAK64768	Primer Atlp Eco/Sp
964	17	0.7	34	19	AAV32357	peni gene downstre
965	17	0.7	34	19	AAV18475	TAI antibody downs
966	17	0.7	34	20	AAK25906	B.licheniformis pe
967	17	0.7	34	21	AAA06164	CFMR gene analysis
968	17	0.7	35	17	AAK31127	Probe Max 277. Sy
969	17	0.7	35	19	AAV27587	Helicobacter pylor
970	17	0.7	35	21	AAZ59523	Hybridisation prob
971	17	0.7	35	22	AAK58535	Cross-linking prob
972	17	0.7	36	17	AAK34758	PCR primer JIA007
973	17	0.7	36	18	AAK86982	Primer used in MHC
974	17	0.7	36	20	AAK15629	Reverse PCR primer
975	17	0.7	36	22	AAK44264	Neisseria meningit
976	17	0.7	36	24	AAK21099	Synthetic oligonuc
977	17	0.7	36	24	ABA01432	Micotiana tabacum
978	17	0.7	37	14	AAQ33350	KHCY cDNA fragment
979	17	0.7	37	15	AAQ73209	Primer PK8978AL to
980	17	0.7	37	19	AAV85646	LRP5 exon primer E
981	17	0.7	37	20	AAK79801	PCR primer FL4529
982	17	0.7	38	13	AAQ35811	HIV-1 gp120 3' reg
983	17	0.7	38	14	AAQ35391	PCR primer HIVM18
984	17	0.7	38	14	AAQ47078	HIV ENV gene PCR p
985	17	0.7	38	17	AAK35819	Primer #8 for prot
986	17	0.7	38	20	AAZ10378	PCR primer used to
987	17	0.7	38	22	AAH96805	Human CHK1 ribozym
988	17	0.7	38	22	AAH96825	Human CHK1 ribozym
989	17	0.7	38	23	ABK05697	Human NCOG zinzyme
990	17	0.7	38	23	ABK05791	Human NCOG zinzyme
991	17	0.7	38	23	ABK05792	Human NCOG zinzyme
992	17	0.7	38	23	ABK05800	Human NCOG zinzyme
993	17	0.7	38	23	ABK05873	Human NCOG zinzyme
994	17	0.7	38	24	ABK21101	Human ERG G-leave
995	17	0.7	39	20	AAZ28764	G-less oligonucleo
996	17	0.7	39	21	AAK62594	Human E6-AP lower
997	17	0.7	39	22	AAK91503	Chr gene/PorA prom
998	17	0.7	39	24	AAK47046	Rev-binding sequen
999	17	0.7	39	24	ABK37886	Promoter replaceme
1000	17	0.7	40	19	AAV31611	Nucleotide sequenc

## ALIGNMENTS

## RESULT 1

AAK27799/C  
ID AAL27799 standard; DNA: 50 BP.

AC AAL27799;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #1007.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX	28-DEC-1999;	99US-0173419.
PR	27-DEC-2000;	2000US-0173419.
XX	(CURA-) CURAGEN CORP.	
PA	Shinkels RA, Leach M;	
PI	WPI; 2001-465210/50.	
DR		
XX		
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,	
PT	oncogenes and histones, useful for diagnosing and treating, e.g.	
PT	cancer, autoimmune diseases and infections -	
XX		
PS	Claim 1: Page 1667; 4143p; English.	
XX		
CC	The present invention relates to oligonucleotides encoding polymorphic	
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,	
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,	
CC	histones, kinases, colony stimulating factors, complement related	
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,	
CC	G-protein coupled receptors and thioesterases. The present sequence is	
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded	
CC	by them may be used in the prevention, diagnosis and treatment of	
CC	diseases associated with inappropriate expression of the proteins listed	
CC	above. Disorders that may be prevented, diagnosed and/or treated include	
CC	multifactorial diseases with a genetic component, such as autoimmune	
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,	
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer	
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,	
CC	leukaemia), diseases of the nervous system and an infection of pathogenic	
CC	organisms.	
XX		
SO	Sequence 50 BP; 20 A; 11 C; 8 G; 11 T; 0 other;	

Query Match 2.2%; Score 50; DB 22; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.0042;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1074 TCAATTCACACGAGGAAACTTTCGTCGTCCTTTGTTCTCGAATT 1123

DB 50 TGATTCACACGAGGAAACTTTCGTCGTCCTTTGTTCTCGAATT 1

## RESULT 2

AAK27796/C  
ID AAL27796 standard; DNA: 50 BP.

AC AAL27796;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #1004.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

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XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX PT cancer, autoimmune diseases and infections.
XX PS Claim 1; Page 1667; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX CC G-protein coupled receptors and thioesterases. The present sequence is
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX CC by them may be used in the prevention, diagnosis and treatment of
XX CC diseases associated with inappropriate expression of the proteins listed
XX CC above. Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney/
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms.
XX SQ Sequence 50 BP; 10 A; 10 C; 10 G; 20 T; 0 other;

Query Match 1.7%; Score 39; DB 22; Length 50;
Best Local Similarity 98.0%; Pred. No. 2.7;
Matches 50; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1313 GGCAGAAAGATCCCATGTTGACAAACACAGCCAGGGGATATTACT 1363
DB 50 GGCAGAAAGATCCCATGTTGAC-AAACACAGCCAGGGGATATTACT 1

RESULT 3
ABK67234/C
ID ABK67234 standard; DNA: 28 BP.
XX AC ABK67234;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #1322.
XX DE Primer: ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-0225928.
XX PR 21-MAY-1997; 97US-0859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Johndaze G, Bibilashvili R;
XX DR WPI; 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analysing
XX PT differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers

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PS Example 3; SEQ ID No 1322; 11pp; English.
XX CC The invention relates to producing a sub-population of labeled nucleic
XX CC acids (NAs) comprising contacting a NA sample from a physiological
XX CC source, with a pool of 50 distinct gene specific primers under suitable
XX CC conditions to enzymatically generate sub-population of NAs, where
XX CC each gene specific primer has a sequence complementary to a distinct
XX CC mRNA, and each labeled NA is generated using a single gene specific
XX CC primer. The method is useful for producing a sub-population of labeled
XX CC NAs which is useful for analysing the differences in the RNA profiles
XX CC between several different physiological sources, where the method
XX CC comprises producing subpopulation of labeled NAs for each physiological
XX CC source to identify differences in the population, where the comparison
XX CC is preferably performed by hybridising the labeled NAs for each of the
XX CC distinct physiological sources to an array of probe NAs stably
XX CC associated with the surface of a substrate to produce a hybridisation
XX CC pattern for each of the sources, and comparing the patterns for each of
XX CC the sources, where differential gene expression assays are
XX CC utilised in differential expression analysis of diseased a normal
XX CC tissue e.g. neoplastic a normal tissue, or different tissue or
XX CC sub-tissue types. The present sequence is a human gene specific PCR
XX CC primer used in the method of the invention.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from USPTO at
XX CC http.wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.
XX SQ Sequence 28 BP; 8 A; 5 C; 9 G; 6 T; 0 other;

Query Match 1.2%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 CTTTGACTCTCAGTCGATGACCCACAC 886
DB 28 CTTTGACTCTCAGTCGATGACCCACAC 1

RESULT 4
AAF27845
ID AAF27845 standard; DNA: 29 BP.
XX AC AAF27845;
XX DT 02-MAY-2001 (first entry)
XX DE Mutagenic upper primer used to generate human caspase-7 mutant C186S.
XX DE Human; apoptotic; nuclear factor-kappa B; NF-kB; Jun N-terminal kinase;
XX DE JUNK; apoptosis; Caspase-7; caspase-8; mutant; mutagenic primer; ss.
XX OS Homo sapiens.
XX PN US6160095-A.
XX PD 12-DEC-2000.
XX PF 24-AUG-1999; 99US-0382155.
XX PR 07-MAY-1998; 98US-0074044.
XX PA (UNIW ) UNIV WASHINGTON.
XX PA (STOW-) STOWERS INST MEDICAL RES.
XX PI Hood L, Chaudhary PM;
XX DR WPI; 2001-101569/11.
XX PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
XX PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
XX PT for therapeutic purposes

```

PS Disclosure; Column 14; 60pp; English.  
 CC The present sequence was used to generate a mutant of a human caspase.  
 CC Three novel mutants (D73A, L74A and L75A) for Caspase-8 were also made.  
 CC These are useful for regulating NF-kB, JNK and apoptosis activities.  
 CC The Caspase-8 mutants are useful for therapeutic purposes and in test  
 CC methods or assays for determining whether a candidate compound has a  
 CC significant effect upon cell activities, especially NF-kB, JNK and  
 CC apoptosis, so as to facilitate the discovery and/or design of therapeutic  
 CC agents.  
 CC  
 SQ Sequence 29 BP; 6 A; 8 C; 9 G; 6 T; 0 other;  
 Query Match 1.2%; Score 27.4; DB 22; Length 29;  
 Best Local Similarity 96.6%; Pred. No. 2e+03;  
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 585 TCTTCATTCAGGCTGCGAGGACCGAG 613  
 Db 1 TCTTCATTCAGGCTGCGAGGACCGAG 29

RESULT 5  
 AAF27846/C  
 ID AAF27846 standard; DNA; 29 BP.  
 AC AAF27846;  
 XX  
 DT 02-MAY-2001 (first entry)  
 DE Mutagenic lower primer used to generate human caspase-7 mutant C186S.  
 XX  
 DE Human; apoptotic; nuclear factor-kappa B; NF-kB; Jun N-terminal kinase;  
 KW JNK; apoptosis; Caspase-7; caspase-8; mutant; mutagenic primer; ss.  
 OS Homo sapiens.  
 XX  
 OS US6160095-A.  
 PN 12-DEC-2000.  
 PD 24-AUG-1999; 99US-0382155.  
 PF 07-MAY-1998; 98US-0074044.  
 PR (UNIV ) UNIV WASHINGTON.  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 XX  
 PI Hood L, Chaudhary PM;  
 XX  
 DR WPI; 2001-101569/11.  
 DR  
 PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating  
 PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,  
 PT for therapeutic purposes -  
 PS Disclosure; Column 14; 60pp; English.  
 XX  
 CC The present sequence was used to generate a mutant of a human caspase.  
 CC Three novel mutants (D73A, L74A and L75A) for Caspase-8 were also made.  
 CC These are useful for regulating NF-kB, JNK and apoptosis activities.  
 CC The Caspase-8 mutants are useful for therapeutic purposes and in test  
 CC methods or assays for determining whether a candidate compound has a  
 CC significant effect upon cell activities, especially NF-kB, JNK and  
 CC apoptosis, so as to facilitate the discovery and/or design of therapeutic  
 CC agents.  
 CC  
 SQ Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 other;

Query Match 1.2%; Score 27.4; DB 22; Length 29;  
 Best Local Similarity 96.6%; Pred. No. 2e+03;  
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCTTCATTCAGGCTGCGAGGACCGAG 613  
 Db 29 TCTTCATTCAGGCTGCGAGGACCGAG 1

RESULT 6  
 AAF87626  
 ID AAF87626 standard; DNA; 29 BP.  
 AC AAF87626;  
 XX  
 DT 12-JUL-2001 (first entry)  
 DE Upper primer for generation of Caspase 7 mutant C186S.  
 XX  
 DE NF-kappaB, JNK; apoptosis; death effector domain; DED; primer; ss.  
 KW  
 OS Homo sapiens.  
 OS US6207458-B1.  
 PN 27-MAR-2001.  
 PD 07-MAY-1998; 98US-0074044.  
 PF 07-MAY-1998; 98US-0074044.  
 PR 07-MAY-1998; 98US-0074044.  
 XX  
 PA (UNIV ) UNIV WASHINGTON.  
 XX  
 PI Chaudhary PM, Hood L;  
 XX  
 DR WPI; 2001-342087/36.  
 DR  
 PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis  
 PT activity by comparing cell activity in presence and absence of  
 PT proteinaceous species having two death effector domain and test  
 PT compound -  
 PS Disclosure; Column 14; 62pp; English.  
 CC  
 CC The present invention relates to testing candidate compounds to  
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.  
 CC The method involves the use of 2 death effector domains (DED). The  
 CC compounds identified by the invention have therapeutic  
 CC applications and are useful for regulating cellular NFkappaB, JNK  
 CC and apoptosis activity. The assay is useful for identifying  
 CC pharmacological agents or lead compounds generally involved in  
 CC assaying for compounds which regulate or modulate a cell activity.  
 CC The present sequence is a primer used in the invention.  
 CC  
 SQ Sequence 29 BP; 6 A; 8 C; 9 G; 6 T; 0 other;

Query Match 1.2%; Score 27.4; DB 22; Length 29;  
 Best Local Similarity 96.6%; Pred. No. 2e+03;  
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCTTCATTCAGGCTGCGAGGACCGAG 613  
 Db 1 TCTTCATTCAGGCTGCGAGGACCGAG 29

RESULT 7  
 AAF87627/C  
 ID AAF87627 standard; DNA; 29 BP.  
 AC AAF87627;  
 XX  
 DT 12-JUL-2001 (first entry)  
 DE Lower primer for generation of Caspase 7 mutant C186S.  
 DE NF-kappaB, JNK; apoptosis; death effector domain; DED; primer; ss.  
 KW  
 XX

Query Match 1.2%; Score 27.4; DB 22; Length 29;  
 Best Local Similarity 96.6%; Pred. No. 2e+03;  
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OS Homo sapiens.
XX
XX US6207458-B1.
XX
XX 27-MAR-2001.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Chaudhary PM, Hood L;
XX
XX WPI; 2001-342087/36.
XX
XX Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
XX activity by comparing cell activity in presence and absence of
XX PT proteaseous species having two death effector domain and test
XX compound
XX
XX Disclosure; Column 14; 62pp; English.
XX
XX The present invention relates to testing candidate compounds to
XX determine whether they affect NF-kappaB, JNK and apoptosis activity.
XX The method involves the use of 2 death effector domains (DED). The
XX CC The compounds identified by the invention have therapeutic
XX applications and are useful for regulating cellular NFkappaB, JNK
XX and apoptosis activity. The assay is useful for identifying
XX CC pharmacological agents or lead compounds generally involved in
XX CC assaying for compounds which regulate or modulate a cell activity.
XX The present sequence is a primer used in the invention.
XX
XX Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 27.4; DB 22; Length 29;
Best Local Similarity 96.6%; Pred. No. 2e+03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 585 TCTTCATTGAGGCTTCCGAGGACCGAG 613
DB 29 TCTTCATTGAGGCTTCCGAGGACCGAG 1
RESULT 8
ABN80828
ID ABN80828 standard; DNA: 27 BP.
XX
XX ABN80828;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human caspase 7 PCR probe SEQ ID NO:6.
XX
XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX hyperproliferative disorder; cancer; bone metabolism; infection;
XX cholesterol disorder; inflammation; tumour; PCR probe; ss.
XX
XX Homo sapiens.
XX
XX WO200222640-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28232.
XX
XX 11-SEP-2000; 2000US-0659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX

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DR WPI; 2002-401902/43.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX PT for modulating gene expression and treating diseases associated with
XX PT expression of caspase 7 in humans
XX
XX Example 13; Page 82; 138pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in
XX length targeted to a nucleic acid molecule encoding caspase 7, which
XX specifically hybridises with and inhibits the expression of caspase 7.
XX (I) has antiinflammatory and cytostatic activities, and can be used in
XX antisense therapy and as an inhibitor of caspase 7 expression. (I) is
XX useful for inhibiting the expression of caspase 7 in human cells or
XX tissues, and for treating a human having a disease or condition
XX associated with caspase 7 including inflammatory condition,
XX hyperproliferative disorder (cancer), or bone metabolism or cholesterol
XX disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
XX as research reagent and kits. (I) is useful prophylactically to prevent
XX CC or delay infection, inflammation or tumour formation. The present
XX CC sequence represents a PCR probe for human caspase 7, which is used in
XX CC an example from the present invention.
XX
XX Sequence 27 BP; 10 A; 6 C; 5 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 27; DB 24; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1305 TTGCACTTGCAAAAAGAAATCCCAATG 1331
DB 1 TTGCACTTGCAAAAAGAAATCCCAATG 27
RESULT 9
ABK67138/C
ID ABK67138 standard; DNA: 27 BP.
XX
XX ABK67138;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human gene specific PCR primer #1226.
XX
XX Primer; ss; DNA microarray; differential expression analysis; human.
XX
XX Homo sapiens.
XX
XX US6352829-B1.
XX
XX 05-MAR-2002.
XX
XX 05-JAN-1999; 99US-0225928.
XX
XX 21-MAY-1997; 97US-0859998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Jokhadze G, Bibilashvili R;
XX
XX WPI; 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analysing
XX PT differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers
XX
XX Example 3; SEQ ID No 1226; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
XX CC acids (NAs) comprising contacting a NA sample from a physiological
XX CC source, with a pool of 50 distinct gene specific primers under suitable
XX CC conditions to enzymatically generate sub-population of NAs, where
XX each gene specific primer has a sequence complementary to a distinct

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CC utilised in differential expression analysis of diseased a normal  
 CC tissue e.g. neoplastic a normal tissue, or different tissue or  
 CC subltissue types. The present sequence is a human gene specific PCR  
 CC primer used in the method of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from USPTO at  
 CC http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.

XX Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 other;  
 SQ

Query Match 1.1%; Score 26; DB 24; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 TGTTCACACCCAGGCGTATGAGA 1630  
 Db 1 TGTTCACACCCAGGCGTATGAGA 26  
 |||||||||||||||||||

RESULT 12  
 ABR67233  
 ID ABR67233 standard; DNA; 26 BP.  
 XX  
 AC ABR67233;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human gene specific PCR primer #1321.  
 DE  
 KW Primer; ss; DNA microarray; differential expression analysis; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US6352829-B1.  
 PN  
 PD 05-MAR-2002.  
 PD  
 XX 05-JAN-1999; 99US-0225928.  
 PE  
 XX 21-MAY-1997; 97US-0859998.  
 PR  
 PA (CLON-) CLONTECH LAB INC.  
 PA  
 PI Chenchik A, Jekhadze G, Biblilashvili R;  
 PI  
 DR WPI; 2002-314699/35.  
 DR  
 XX Producing sub-population of labeled nucleic acids, useful for analysing  
 PT differences in RNA profiles between several different physiological  
 PT sources, using set of distinct gene specific primers -  
 PT  
 XX Example 3; SEQ ID No 1321, 11pp; English.  
 PS  
 XX The invention relates to producing a sub-population of labeled nucleic  
 CC acids (NAs) comprising contacting a NA sample from a physiological  
 CC source, with a pool of 50 distinct gene specific primers under suitable  
 CC conditions to enzymatically generate sub-population of NAs, where  
 CC each gene specific primer has a sequence complementary to a distinct  
 CC mRNA, and each labeled NA is generated using a single gene specific  
 CC primer. The method is useful for producing a sub-population of labeled  
 CC NAs which is useful for analysing the differences in the RNA profiles  
 CC between several different physiological sources, where the method  
 CC comprises producing subpopulation of labeled NAs for the different  
 CC physiological sources, comprising the populations for each physiological  
 CC source to identify differences in the population, where the comparison  
 CC is preferably performed by hybridising the labeled NAs for each of the  
 CC distinct physiological sources to an array of probe NAs stably  
 CC associated with the surface of a substrate to produce a hybridisation  
 CC pattern for each of the sources, and comparing the patterns for each of  
 CC the sources, where differential gene expression assays are  
 CC utilised in differential expression analysis of diseased a normal  
 CC tissue e.g. neoplastic a normal tissue, or different tissue or

CC subltissue types. The present sequence is a human gene specific PCR  
 CC primer used in the method of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from USPTO at  
 CC http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.

XX Sequence 26 BP; 4 A; 7 C; 7 G; 8 T; 0 other;  
 SQ

Query Match 1.1%; Score 26; DB 24; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGGCTTGCCGAGGAC 609  
 Db 1 TTCTTCATTCAGGCTTGCCGAGGAC 26  
 |||||||||||||||||||

RESULT 13  
 AAD13077/C  
 ID AAD13077 standard; DNA; 48 BP.  
 XX  
 AC AAD13077;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Mammalia caspase-3 cDNA amplifying PCR primer, C33.  
 DE  
 XX Protein destabilisation: linker moiety; reporter moiety; disease model;  
 KW linear multimerised domain; -NH-ubiquitin protein endoprotease;  
 KW transgenic animal; transgenic plant; disease resistance;  
 KW caspase-3; PCR primer; ss.  
 KW  
 XX Mammalia.  
 OS  
 XX WO200157242-A2.  
 PN  
 PD 09-AUG-2001.  
 PD  
 XX 02-FEB-2001; 2001WO-US03791.  
 PE  
 XX 04-FEB-2000; 2000US-0498098.  
 PR  
 PA (AURO-) AURORA BIOSCIENCES CORP.  
 PA  
 PI Stack JH, Whitney M, Cubitt AB, Pollack BA;  
 PI  
 DR WPI; 2001-488890/53.  
 DR  
 XX Destabilizing proteins in living cells, by coupling a target protein to  
 PT linear multimerized destabilization domain non-cleavable by  
 PT -NH-ubiquitin protein endoproteases, comprising two copies of the  
 PT domain -  
 PT  
 XX Example 4; Page 132; 171pp; English.  
 PS  
 XX The present invention relates to a method for destabilising a target  
 CC protein in a cell. The method comprises a linker moiety which operatively  
 CC couples a target protein (a reporter moiety) to a linear multimerised  
 CC destabilising domain, which is non-cleavable by a -NH-ubiquitin protein  
 CC endoproteases. The method is useful for detecting an activity such as  
 CC protease, protein kinase or phosphoprotein phosphatase activity and is  
 CC also useful for identifying modulators of these activities. The method  
 CC is also useful for developing novel assays for a wide range of  
 CC post-translational activities, such as proteolysis, phosphorylation,  
 CC dephosphorylation, glycosylation, methylation, sulfation, prenylation,  
 CC disulfide bond formation and ADP-ribosylation within cells. The  
 CC recombinant DNA molecule of the invention is useful for creating  
 CC transgenic animals useful as disease models and transgenic plants with  
 CC improved disease resistance or other favourable traits. The present  
 CC sequence is a PCR primer which is used for the amplification of mammaia  
 CC caspase-3 cDNA, used as a reporter moiety in the exemplification of  
 CC the invention.

```

Query Match          1.1%; Score 25; DB 21; Length 47;
Best Local Similarity 75.6%; Pred. No. 1e+04;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0

QY 1504 GTCTGGAAACAGAACCATTCATTCAGTGTTCCAAACAGAGG 1544
      11 ||||| ||||| ||||| ||||| ||||| ||||| |||||
      4 GTGAGGAACAGCAAAACACGCTAGTATTTCAAAACAAGTG 44

Db

RESULT 15
AAZ25254
ID AAZ25254 standard; DNA; 42 BP.
AC AAZ25254;
XX
DT 15-DEC-1999 (first entry)
XX
DE Caspase-3 PCR primer SEQ ID NO:10.
XX
KW Apoptosis; regulation; chemically induced dimerisation; aggregation;
KW artificial death switch; AD5; cysteine protease; caspase-1; ICE;
KW caspase-3; YAMA; FK506-binding protein; FKBP; development;
KW hyperproliferative disorder; tumour; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO950425-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06799.
XX
PR 30-MAR-1998; 98US-0079831.
XX
PA (BAYU ) BATLOR COLLEGE MEDICINE.
XX
PI Spencer DM, Slawin KM;
XX
DR WPI; 1999-591323/50.
XX
PT Conditionally lethal artificial death switches based on chemically
PT induced dimerisation of cysteine proteases - useful for treating
PT hyperproliferative diseases
XX
PS Example 1; Page 20; 117pp; English.
XX
CC The present invention describes a conditionally lethal molecule (A)
CC comprising a chemical inducer binding domain and an apoptosis inducing
CC factor, where the apoptosis inducing factor is an apoptosis signal
CC transducing factor. A vector encoding (A) is useful for treating a
CC disease, e.g. a hyperproliferative disease that is benign or malignant,
CC or atherosclerosis. The nucleotide sequence (I) encoding (A) can be
CC used to cause regression of a tumour, reduction in tumour size or
CC reduction in PSA levels, by transfecting the nucleic acid into cells of
CC the tumour. (I) can also be used to affect the rate of cell proliferation
CC caused by BPH by transfecting (I) into prostate cells. (I) is also used
CC to induce apoptosis in a cell as well as for determining the biological
CC role of a cell type. The conditionally lethal gene is non-toxic unless
CC induced. It does not require membrane localisation and bypasses
CC endogenous apoptosis control mechanisms. The present sequence represents
CC a PCR primer used in an example from the present invention.
XX
XX
SQ Sequence 42 BP; 8 A; 11 C; 13 G; 10 T; 0 other;

Query Match          1.1%; Score 24.4; DB 20; Length 42;
Best Local Similarity 73.8%; Pred. No. 1.4e+04;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 590 ATTCAAGCTTGCAGAGGACGACGATTGATATGTCACATCCAG 631
      11 ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1 ATTCAAGCTTCCCGTGTACCGAAGTGCACGTGTGCATTGAG 42

```



PD 30-OCT-1997.  
 XX  
 PF 10-APR-1997; 97WO-FR00636.  
 XX  
 PR 25-APR-1996; 96FR-0005223.  
 XX  
 PA (RHON ) RHONE-POULENC RORER SA.  
 XX  
 PI Mallet J, Meloni R, Ravassard P, Trelhou F;  
 XX WPI: 1997-549358/50.  
 DR  
 XX  
 PT Transcription enhancers derived from first intron of tyrosine  
 PT hydroxylase gene - useful in expression vectors for producing  
 PT proteins especially for gene therapy  
 XX  
 PS Claim 6; Page 21; 42pp; French.

CC This sequence represents a specifically claimed DNA fragment derived  
 CC from the first intron of the tyrosine hydroxylase gene containing an  
 CC allele of the HUMTHOI microsatellite. The invention relates to a new  
 CC isolated DNA fragment (A) which has transcription enhancing activity and  
 CC is defined as: (a) consisting of part of the first intron of the  
 CC tyrosine hydroxylase (TH) gene, especially an allele of the HUMTHOI  
 CC microsatellite; or (b) possessing the sequence (1): (TCAT)n-(CAT)o-  
 CC (TCAT)p (1) n = 1-50; o = 0-20; and p = 0-50. The new enhancers are  
 CC incorporated into expression cassettes and plasmid or viral vectors for  
 CC expressing proteins in vitro, in vivo or ex vivo. They are especially  
 CC intended for use in mammalian cells for gene therapy, e.g. of cancer or  
 CC restenosis.  
 XX  
 SO Sequence 41 BP; 9 A; 14 C; 0 G; 18 T; 0 other;

Query Match 1.0%; Score 22.8; DB 18; Length 41;  
 Best Local Similarity 79.4%; Pred. No. 3.5e+04;  
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1978 CTCACAAATTTATCCATTCATTCATTTATTCATT 2011  
 DB 3 CTCATTCATTCATTCATTCATTCATTCATTCATT 36

RESULT 19  
 AAT66978/C  
 ID AAT66978 standard; DNA; 30 BP.  
 XX  
 AC AAT66978;  
 XX  
 XX

DT 21-JUL-1997 (first entry)

DE Cysteine protease CMH-1 PCR primer.

XX Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;  
 KW programmed cell death; cancer; neurodegenerative disease;  
 KW autoimmune disease; gene therapy; diagnosis; primer; PCR;  
 KW polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 XX

PN WO9716552-A1.

PD 09-MAY-1997.

PF 01-NOV-1996; 96WO-US17431.

PR 16-NOV-1995; 95US-0558733.

PR 03-NOV-1995; 95US-0007211.

PR 06-NOV-1995; 95US-0007251.

PA (VERT-) VERTEX PHARM INC.  
 XX  
 PI Lipke JA, Su M;  
 XX

DR WPI: 1997-272121/24.

XX  
 XX DNA encoding active, activatable or inactive cysteine protease CMH-1  
 PT - useful in gene therapy for promoting and inhibiting apoptosis and  
 PT for diagnosing cells with potential for apoptosis  
 XX  
 PS Example 3; Page 25; 48pp; English.

XX PCR primers (AAT66977-78) were designed to introduce in-frame XhoI  
 CC sites to the 5' and 3' ends of human cysteine protease cmh-1  
 CC cDNA (see also AAT66970). The PCR product XhoI fragment was ligated  
 CC into pET-15b inducible E. coli expression vector. The resulting  
 CC plasmid encoded a polypeptide comprising a 23-residue N-terminal  
 CC peptide (AAW15248) cony. a hexanistidine tag and thrombin cleavage  
 CC site, fused to Ala24 of CMH-1. Hexanistidine-tagged CMH-1 (Ala24-  
 CC Gln303) was produced in E. coli BM21 (DE3) transformants.  
 XX

SQ Sequence 30 BP; 7 A; 5 C; 10 G; 8 T; 0 other;

Query Match 1.0%; Score 22; DB 18; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 935 GAACCTCTACTCAGTCATATAGC 956  
 DB 30 GAACCTCTACTCAGTCATATAGC 9

RESULT 20  
 AAL30903/C  
 ID AAL30903 standard; DNA; 50 BP.  
 XX  
 AC AAL30903;  
 XX  
 DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #4111.  
 XX  
 XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neutrotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200147944-A2.  
 PN  
 XX  
 PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;  
 XX  
 XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1; Page 2567; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX  
SQ Sequence 50 BP; 10 A; 17 C; 18 G; 5 T; 0 other;

Query Match 1.0%; Score 22; DB 22; Length 50;  
Best Local Similarity 67.4%; Pred. No. 6.1e+04;  
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 92 GCAATGAGATGTCAGTCAAGCCAGACCGGTCCTGTTG 137  
DB 49 GCAGGTAGGCTTCAGGGATGCTGGCCACGCTGCCCTCCGCTG 4

RESULT 21  
AAI76189/c  
ID AAI76189 standard; DNA: 50 BP.  
XX  
AC AAI76189;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:3130.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US32758.  
XX  
PR 30-NOV-1999; 99US-0168138.  
PR 29-NOV-2000; 2000US-0726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
FI Shinkets RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy -  
XX  
PS Claim 1; Page 1008; 2653pp; English.  
XX  
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides.  
CC For example, (I) may be used to treat disorders by rectifying mutations  
CC or deletions in a patient's genome that affect the activity of  
CC polypeptides by expressing inactive proteins or to supplement the  
CC patients own production of polypeptide. Additionally, (I) and its  
CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids  
CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (I) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.

XX  
SQ Sequence 50 BP; 9 A; 21 C; 11 G; 9 T; 0 other;

Query Match 1.0%; Score 22; DB 22; Length 50;  
Best Local Similarity 67.4%; Pred. No. 6.1e+04;  
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1473 AATGATCTGATATGATATCATCCAGATCCAGTCCGAAACAGAA 1518  
DB 48 ACTGCTACTGCTGTGCTGCTGCAGATCCAGGTCACACAGCAGAA 3

RESULT 22  
AAV06634  
ID AAV06634 standard; DNA: 37 BP.  
XX  
AC AAV06634;  
XX  
DT 15-MAY-1998 (first entry)  
XX  
DE Transcription enhancer derived from tyrosine hydroxylase (TH-sense).  
XX  
KW Transcription enhancer; tyrosine hydroxylase; HUMTHO1 microsatellite;  
KW gene therapy; cancer; restenosis; protein expression; ds.  
XX  
OS Synthetic.  
XX  
PN WO9740172-A1.  
XX  
PD 30-OCT-1997.  
XX  
PF 10-APR-1997; 97WO-FR00636.  
XX  
PR 25-APR-1996; 96FR-0005223.  
XX  
PA (RHON ) RHONE-POULENC RORER SA.  
XX  
PI Mallet J, Meloni R, Ravassard P, Trellhou F;  
XX  
FI Mallet J, Meloni R, Ravassard P, Trellhou F;  
XX  
DR WPI; 1997-549358/50.  
XX  
PT Transcription enhancers derived from first intron of tyrosine  
PT hydroxylase gene - useful in expression vectors for producing  
PT proteins especially for gene therapy  
XX  
PS Claim 6; Page 22; 42pp; French.  
XX  
CC This sequence represents a specifically claimed DNA fragment derived  
CC from the first intron of the tyrosine hydroxylase gene containing an  
CC allele of the HUMTHO1 microsatellite. The invention relates to a new  
CC isolated DNA fragment (A) which has transcription enhancing activity and  
CC is defined as: (a) consisting of part of the first intron of the  
CC tyrosine hydroxylase (TH) gene, especially an allele of the HUMTHO1  
CC microsatellite; or (b) possessing the sequence (I): (TCAT)n-(CAT)o-  
CC (TCAAT)p (I) n = 1-50; o = 0-20; and p = 0-50. The new enhancers are  
CC incorporated into expression cassettes and plasmid or viral vectors for  
CC expressing proteins in vitro, in vivo or ex vivo. They are especially  
CC intended for use in mammalian cells for gene therapy, e.g. of cancer or  
CC restenosis.

XX  
SQ Sequence 37 BP; 8 A; 13 C; 0 G; 16 T; 0 other;

Query Match 0.9%; Score 21.8; DB 18; Length 37;  
Best Local Similarity 78.8%; Pred. No. 6e+04;  
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;



XX	Synthetic.	
XX	XX	
PN	MO200234771-A2.	
XX	XX	
PD	02-MAY-2002.	
XX	XX	
PF	29-OCT-2001; 2001WO-GB04789.	
XX	XX	
PR	27-OCT-2000; 2000GB-0026333.	
PR	24-NOV-2000; 2000GB-0028727.	
PR	07-MAR-2001; 2001GB-0005640.	
XX	XX	
PA	(CHIR-) CHIRON SPA.	
PA	(GENO-) INST GENOMIC RES.	
PI	Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;	
PI	Tettein H;	
XX	XX	
DR	WPI: 2002-352536/38.	
XX	XX	
PT	New Streptococcus protein for the treatment or prevention of infection	
PT	or disease caused by Streptococcus bacteria, such as meningitis, and	
PT	for detecting a compound that binds to the protein -	
XX	XX	
PS	Claim 8; Page 4492; 4525pp; English.	
XX	XX	
CC	The invention relates to a protein (ABP25413-ABP30895) from group B	
CC	streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS	
CC	(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in	
CC	the specification. The proteins have antibacterial and antiinflammatory	
CC	activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and	
CC	antibodies that bind (1) are used in the manufacture of medicaments for	
CC	the treatment or prevention of infection or disease caused by	
CC	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.	
CC	Nucleic acids encoding (1) are used to detect Streptococcus in a	
CC	biological sample. (1) is used to determine whether a compound binds to	
CC	(1). A composition comprising (1) or a nucleic acid encoding (1), may be	
CC	used as a vaccine or diagnostic composition. The disease caused by	
CC	Streptococcus that is prevented or treated may be meningitis. Nucleic	
CC	acid encoding (1) may be used to recombinantly produce (1) and may be	
CC	used in gene therapy. Antibodies to (1) are used for affinity	
CC	chromatography, immunoassays, and distinguishing/identifying	
CC	Streptococcus proteins. The present sequence is that of a PCR primer,	
CC	useful to the invention.	
XX	XX	
SQ	Sequence 49 BP; 23 A; 9 C; 10 G; 7 T; 0 other;	
XX	XX	
Query Match	0.9%; Score 21.8; DB 24; Length 49;	
Best Local Similarity	70.7%; Pred. No. 6.8e+04;	
Matches 29; Conservative	0; Mismatches 12; Indels	0; Gaps 0;
OY	2100 TTTTTCAGTTATTTCCAGCCTTATTTGATGTAATATTGT 2140	
Db	45 TTTTGTGATTGTTCAGAGCCCTCTTTTGTGACAAACTTGT 5	
RESULT 26		
ID	AAT78315	
AC	AAT78315 standard; DNA; 49 BP.	
XX	XX	
DT	13-OCT-1997 (first entry)	
XX	XX	
DE	Plasmid vector pZgt-a construction oligonucleotide elpl.21.	
XX	XX	
KW	Recombinant eukaryotic cytoplasmic DNA virus; vaccine production;	
KW	double selection marker; attenuated live pox virus; HIV; HBV;	
KW	surface antigen gene; encephalitis; tick-borne; ss.	
XX	XX	
OS	Synthetic.	
XX	XX	
PN	EP753561-A1.	

PD	XX	15-JAN-1997.
XX	Pf	10-JUL-1995; 95EP-0110727.
XX	Pf	10-JUL-1995; 95EP-0110727.
PR	PR	10-JUL-1995; 95EP-0110727.
XX	PA	(IMMO ) IMMUNO AG.
XX	PI	Antoine G, Dörner F, Eibl J, Falkner F, Schefflinger F;
XX	DR	WPI, 1997-079382/08.
PT	PT	Prod'n. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
PT	PT	prod'n. - using novel construct contg. foreign DNA and double
XX	PS	selection marker
XX	PS	Example 1; Page 8; 68pp; English.
CC	XX	A method has been produced for the production of recombinant eukaryotic
CC	XX	cytoplasmic DNA viruses for vaccine production. The method involves
CC	XX	inserting a construct DNA molecule into the genome of a eukaryotic
CC	XX	cytoplasmic DNA virus, transfecting cells with the virus, and selecting
CC	XX	a recombinant virus that does not contain the double selection marker
CC	XX	cassette from the construct DNA. The DNA molecule preferably contains
CC	XX	one or more foreign DNA segments of a gene encoding an antigen of a
CC	XX	pathogen (especially HIV env, HIV gag, HIV gpapoli, HIV nef, HBV
CC	XX	presl-S2-S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV
CC	XX	S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
CC	XX	encephalitis E gene), and has a double selection marker cassette which
CC	XX	is flanked by at least two direct repeat DNA sequences, where at least
CC	XX	one foreign DNA segment does not occur within the DNA sequence bounded
CC	XX	by the direct repeat sequences and where the double selection marker
CC	XX	cassette comprises a dominant selection marker gene and a colour
CC	XX	selection marker gene (preferably the colour selection marker is the
CC	XX	Escherichia coli lacZ gene and the dominant selection marker is the
CC	XX	E.coli hph or gpt gene). The present sequence represents the elpl.21
CC	XX	Oligonucleotide used in the construction of the plasmid vector pzopt-a.
CC	XX	The DNA constructs and method are used for the production of vaccines,
XX	XX	especially containing an attenuated live recombinant pox virus.
SQ		Sequence 49 BP; 17 A; 8 C; 3 G; 21 T; 0 other;
		Query Match 0.9%; Score 21.6; DB 18; Length 49;
		Best Local Similarity 68.2%; Pred. No. 7.7e+04;
		Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy		2060 ATGTCGAATAATCTGTATTAGCTTTAAARATATCGAAGCTTTT 2103
Dd		2 ATTGGTAACCTATTATTATAGCATGAAGAATATATTTCAACTTTT 45
RESULT 27		
ID	AAF69254/c	
ID	AAF69254 standard; DNA; 45 BP.	
XX	AAF69254;	
DT	17-APR-2001 (first entry)	
DE	Primer used in affinity-improved anti-IgE antibody generation SEQ ID 27.	
XX	Antibody: antisthmatic; anti allergic; ophthalmological; dermatological;	
KW	antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;	
KW	conjunctivitis; eczema; urticaria; food allergy; ss.	
XX	Synthetic.	
OS		
PN	US6172213-B1.	
BD	09-JAN-2001.	
PF	30-JUN-1998; 98US-0109207.	

```
XX 02-JUL-1997; 97US-0051554.
PR (GETH ) GENENTECH INC.
PA Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI WPI: 2001-122353/13.
DR
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display
PS
XX Example 4: Column 73-74; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody
CC with improved anti-1GE antibody activity. The antibody has improved
CC action due to a process comprising, a) identifying aspartyl residues
CC prone to isomerization in unimproved anti-1GE (immunoglobulin E)
CC antibody; b) substituting alternative residues to create candidate
CC molecules; and c) selecting those candidate molecules which display
CC affinity against the target molecule. Use of the antibody results in
CC antiasthmatic; antiallergic; ophthalmological; dermatological and
CC antiinflammatory activity. The antibodies are useful for treating
CC eczema, urticaria and food allergies. The mutant antibodies produced by
CC the above mentioned nucleic acids may also be used as affinity
CC purification agents and in diagnostic assays for detecting the expression
CC of an antigen of interest in specific cell, tissues or serum. Amino acid
CC sequences AAB76936-AAB76960 represent fragments of anti-1GE antibodies of
CC the invention. Polynucleotide sequence AAF69253 represents an expression
CC plasmid used in the course of the invention, and oligonucleotides
CC - AAF69254 - AAF69271 are used in the generation of affinity improved
CC anti-1GE antibodies.
XX
XX Sequence 45 BP; 15 A; 9 C; 10 G; 11 T; 0 other;
SQ
Query Match 0.9%; Score 21.4; DB 22; Length 45;
Best Local Similarity 71.8%; Pred. No. 8.3e+04;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1201 CTGTTACCTTGTATAGACTTAATACATGCAACAGAG 1239
DB 41 CTATCACCCTTATTAGACTTATTAAGTGCACGACGAC 3
RESULT 28
AAF77140
ID AAF77140 standard; DNA; 48 BP.
XX
XX AAF77140;
AC
XX 22-MAY-2001 (first entry)
DT
XX R-structure nucleotide #9.
DE
XX Resonating; R-structure; tertiary structure; anti-viral; ss.
KM
XX
XX Ebola virus.
OS
XX
XX US6194155-B1.
PN
XX 27-FEB-2001.
PD
XX
XX 05-MAY-1999; 99US-0305408.
PF
XX 05-MAY-1999; 99US-0305408.
PR
XX
XX (COHE/) COHEN J.
PA
XX
XX Cohen J;
PI
XX
```

```
DR WPI: 2001-234428/24.
XX
XX Computerized method for identifying and locating resonating,
PT self-hybridizing nucleic acid elements comprises employing a
PT device, which has computer program instructions for creating data
PT structures and operator modules
PS
XX Example 1; Column 11-12; 21pp; English.
XX
XX The present invention relates to identifying resonating,
CC self-hybridizing molecular genetic nucleotide structures
CC (R-structures) in a nucleic acid sequence, employing a
CC memory device. The method is also useful for identifying
CC viral nucleic acid sequences that form tertiary structures.
CC The ability to identify such structures or sequences may
CC lead to faster development of anti-viral therapies.
XX
XX Sequence 48 BP; 20 A; 7 C; 5 G; 16 T; 0 other;
SQ
Query Match 0.9%; Score 21.4; DB 22; Length 48;
Best Local Similarity 71.8%; Pred. No. 8.6e+04;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1023 CTTTGAATATTTCAGAAATTCCTCCAGATTATTTTC 1061
DB 2 CTTTAAATATTTAAGAAACTGACGACATTAATTC 40
RESULT 29
AAL28758
ID AAL28758 standard; DNA; 50 BP.
XX
XX AAL28758;
AC
XX 24-JAN-2002 (first entry)
DT
XX
XX Human SNP oligonucleotide #1966.
DE
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neutroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinase; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US35498.
PP
XX
XX 28-DEC-1999; 99US-0173419.
PR
XX 27-DEC-2000; 2000US-0173419.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkels RA, Leach M;
PI
XX
XX WPI: 2001-465210/50.
DR
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections
PS
XX Claim 1; Page 1944; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
```



CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX Sequence 50 BP; 21 A; 8 C; 6 G; 15 T; 0 other;

Query Match 0.9%; Score 21.4; DB 22; Length 50;

Best Local Similarity 66.0%; Pred. No. 8.7e+04;

Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1472 TAATGATTCTGATATATCCATCCAGATCCAGTCGGAACAGAA 1518

DB 1 TATACATTCAGATATGTTGAAACATCTTAAGGCTACAAACAGAA 47

RESULT 30

AAH29638

ID AAH29638 standard; DNA; 47 BP.

XX AAH29638;

XX 17-JUL-2001 (first entry)

DE Drosophila melanogaster essential gene fragment, SEQ ID NO: 827.

XX Drosophila melanogaster; fruit fly; essential gene; screening assay;

KW pesticide; crop protection; chromosome 2; ds.

XX Drosophila melanogaster.

XX PN - WO200118547-A1.

XX 15-MAR-2001.

PF 06-SEP-2000; 2000WO-GB03444.

PR 07-SEP-1999; 99GB-0021009.

XX (UNITU ) UNIV GLASGOW.

PI Davies RW, Kaiser K, Yang MY;

XX WPI: 2001-281436/29.

PT Screening assays for used for identifying compounds having a

XX physiological effect on proteins identified as being essential -

PS Claim 1; Page 642; 695pp; English.

XX The present sequence is part of an essential gene from Drosophila  
CC melanogaster. Lack of expression of the protein encoded by this  
CC gene leads to a lethal or semi-lethal phenotype. The invention  
CC relates to 902 nucleic acid sequences from genes encoding proteins  
CC which are thought to be essential, and to a screening assay for  
CC identifying compounds which have a physiological effect on these  
CC proteins. Suitable compounds are useful as pesticides and may be used  
CC in conjunction with other pesticides and herbicides for crop  
CC protection. The gene corresponding to the present sequence is located  
CC on chromosome 2.

XX Sequence 47 BP; 13 A; 6 C; 9 G; 19 T; 0 other;

Query Match 0.9%; Score 21.2; DB 22; Length 47;

Best Local Similarity 69.0%; Pred. No. 9.5e+04;

Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2041 AACATCTGTTTGGCTTATGTCACAAATCTGTATAGCTT 2082

DB 5 AGCCATATTAAGTGTGTAATTTCCAAAGTTGTATAGATT 46

RESULT 31

AAH6939/C

ID AAH6939 standard; DNA; 48 BP.

XX AAH6939;

XX 15-JAN-2001 (first entry)

DE TPX allele oligonucleotide.

XX Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;

KW single nucleotide polymorphism; identification; viral load; probe;

KW genotyping; medical marker diagnostic; primer; target; mutation;

XX genetic disease; ss.

XX Synthetic.

XX WO200049180-A1.

XX 24-AUG-2000.

PF 18-FEB-2000; 2000WO-US04242.

XX 18-FEB-1999; 99US-0252436.

PR 21-JUL-1999; 99US-0358972.

PR 25-AUG-1999; 99US-0383316.

XX (PROM - ) PROMEGA CORP.

XX Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;

PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;

XX WPI: 2000-565377/52.

XX Determining presence or absence of a predetermined endogenous nucleic

PT acid sequence by using an enzyme that depolymerizes the 3' end of an

PT oligonucleotide probe hybridized to a target sequence to release

XX identifier nucleotides

XX Example: Page 338; 389pp; English.

XX The present invention describes a method (M1) for determining the  
CC presence or absence of a predetermined endogenous nucleic acid target  
CC sequence (ENAT). The method comprises hybridizing a probe having an  
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme  
CC that depolymerizes the 3' end of hybridised NA to release the INs.  
CC M1 is used for determining the number of known sequence repeats present  
CC in a nucleic acid target sequence in a nucleic acid sample. The method  
CC is also useful for determining whether a nucleic acid target sequence in  
CC a sample is an allele from a homozygous or heterozygous locus. The  
CC method is also useful for detection of mutations, translocations and  
CC SNPs in nucleic acids (including those associated with genetic disease),  
CC determination of viral load, species identification, sample  
CC contamination, and analysis of forensic samples. AAH6791 to AAH7079  
CC and AAH12817 represent sequence which are used in the exemplification of  
CC the present invention.  
CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given  
CC in the examples, and the SEQ ID NO: and sequences given in the sequence  
CC listing from the present invention.

XX Sequence 48 BP; 18 A; 7 C; 11 G; 12 T; 0 other;

Query Match 0.9%; Score 21.2; DB 21; Length 48;

Best Local Similarity 69.0%; Pred. No. 9.6e+04;

Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;



PR 10-JUL-1995; 95EP-0110727.  
XX (IMMO) IMMUNO AG.  
XX  
PI Antoine G, Dörner F, Eibl J, Falkner F, Scheiflinger F;  
XX WPI, 1997-079382/08.  
DR  
XX  
XX Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine  
PT Prodn. - using novel construct contg. foreign DNA and double  
PT selection marker  
XX  
XX Example 1; Page 8; 68pp; English.  
PS  
XX  
XX A method has been produced for the production of recombinant eukaryotic  
CC cytoplasmic DNA viruses for vaccine production. The method involves  
CC inserting a construct DNA molecule into the genome of a eukaryotic  
CC cytoplasmic DNA virus, transfecting cells with the virus, and selecting  
CC a recombinant virus that does not contain the double selection marker  
CC cassette from the construct DNA. The DNA molecule preferably contains  
CC one or more foreign DNA segments of a gene encoding an antigen of a  
CC pathogen (especially HIV env, HIV gag, HIV gp120, HIV tat, HIV  
CC p15, S1-S2-S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV  
CC S surface antigen gene, tick-borne encephalitis prem gene or tick-borne  
CC encephalitis E gene), and has a double selection marker cassette which  
CC is flanked by at least two direct repeat DNA sequences, where at least  
CC one foreign DNA segment does not occur within the DNA sequence bounded  
CC by the direct repeat sequences and where the double selection marker  
CC cassette comprises a dominant selection marker gene and a colour  
CC selection marker gene (preferably the colour selection marker is the  
CC Escherichia coli lacZ gene and the dominant selection marker is the  
CC E. coli hph or gpt gene). The present sequence represents the elp1.11  
CC oligonucleotide used in the construction of the plasmid vector ppgpt-a.  
CC The DNA constructs and method are used for the production of vaccines,  
CC especially containing an attenuated live recombinant pox virus.  
XX  
SQ Sequence 45 BP; 19 A; 3 C; 8 G; 15 T; 0 other;  
Query Match 0.9%; Score 21; DB 18; Length 45;  
Best Local Similarity 73.0%; Pred. No. 1.1e+05;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 2067 AAATCTGTTAGCTTAAATATATCTGGAACCTTT 2103  
DB 41 AACCTATTATAGCATGAATATATTTTCAACCTTT 5  
RESULT 35  
AAAS6041/C  
ID AAAS6041 standard; DNA; 47 BP.  
XX  
XX AAAS6041;  
XX  
DT 05-SEP-2000 (first entry)  
XX  
XX Plasmid pKK223-3-lacZ construction PCR primer SEQ ID NO:13.  
XX  
XX Escherichia coli; E. coli; randomised peptide library; identification;  
XX stabilised bioactive peptide; synthesis; intracellular selection;  
XX screening; lac operon; protease resistant; peptidease resistant;  
XX Rop protein; glutathione sulphotransferase; thiorodoxin; infection;  
XX maltose binding protein; glutathione reductase; antimicrobial;  
XX antibacterial; PCR primer; ss.  
OS Escherichia coli.  
OS Synthetic.  
XX  
XX WO200022112-A1.  
XX  
XX 20-APR-2000.  
XX  
XX 12-OCT-1999; 99WO-US23731.  
XX  
XX

PR 13-OCT-1998; 98US-0104013.  
PR 14-DEC-1998; 98US-0112150.  
XX  
XX (UIGE-) UNIV GEORGIA RES FOUND INC.  
XX (ALTM/ ALTMAN E.  
XX  
XX Altman E;  
XX  
XX WPI, 2000-317972/27.  
DR  
XX  
XX Identifying recombinantly an antimicrobial bioactive peptide used as a  
PT therapeutic agent involves transforming a host cell with expression  
PT vector with tightly regulable control region and measuring its  
PT inhibition  
XX  
XX Example 1; Page 36; 135pp; English.  
PS  
XX  
XX The present invention describes a method for identifying a bioactive  
CC peptide (BP) involving transforming a cell with an expression vector  
CC comprising a tightly regulable control region operably linked to a  
CC nucleic acid sequence encoding a peptide (P), growing the transformed  
CC cell under conditions that repress expression of (P) and then inducing  
CC its expression which, if is inhibitory to host cell growth is  
CC indicative of BP expression. An antimicrobial peptide from the present  
CC invention, which is stabilised, is used for treating a patient having a  
CC condition treatable with a peptide drug. The stabilised peptides are  
CC also used for inhibiting the growth of a microbe. The new antibacterial  
CC peptides are useful to treat various pathogenic bacteria such as  
CC Staphylococci, Streptococci and Enterococci which are the primary causes  
CC of nosocomial infections. Novel inhibitor peptides identified by the  
CC method can be medical treatments and therapies directed against  
CC microbial infection. Also, these novel inhibitor peptides can be used,  
CC in turn, to identify additional novel antibacterial peptides using a  
CC synthetic approach, and can also be used to elucidate potential new drug  
CC targets. The inhibitor peptide target which is inactivated is identified  
CC using reverse genetics by isolating mutants that are no longer inhibited  
CC by the peptide. These mutants are then mapped in order to precisely  
CC determine the protein target that is inhibited. AAAS6033 to AAAS6106 and  
CC AAAY90964 to AAAY90999 are sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 47 BP; 15 A; 10 C; 10 G; 12 T; 0 other;  
Query Match 0.9%; Score 21; DB 21; Length 47;  
Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 1238 AGTGACTTCGGAGAAAGCTGATGCTGTCCACATGCAATTGCT 1282  
DB 46 AGTGAATCCGTAATCATGTCATGCTGTTCCCTCGACATCAT 2  
RESULT 36  
AAI75434/C  
ID AAI75434 standard; DNA; 50 BP.  
XX  
XX AAI75434;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ.2375.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX protein therapy; vaccine; probe; diagnostic assay; detection;  
XX quantitation; restorative therapy; polymorphic; ds.  
OS Homo sapiens.  
OS  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US32758.  
XX  
XX

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XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX (CURA-) CUNAGEN CORP.
XX Shinkets RA, Leach M;
XX WPI, 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX Claim 1; Page 778; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 50 BP; 20 A; 12 C; 7 G; 11 T; 0 other;
Query Match 0.9%; Score 21; DB 22; Length 50;
Best Local Similarity 73.0%; Pred. No. 1.1e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2171 TATGCAAGATTTTGGCAGCTTTGTTTCAAGATG 2207
| ||||| ||| ||| ||| ||| ||| |||
Db 38 TGTGCAAGATTTTGTGTGTTTAAAGCTG 2

```

RESULT 37  
 AAA60309/C  
 ID AAA60309 standard; DNA: 41 BP.  
 XX  
 AC AAA60309;  
 XX  
 DT 07-DEC-2000 (first entry)  
 XX  
 DE Human HPC2 CDNA exon 10 mutation screening primer SEQ ID NO: 130.  
 XX  
 KW Human; mouse; prostate cancer predisposing gene; HPC2;  
 KW human chromosome 17p; gene therapy; peptide therapy; drug design;  
 KW PCR primer; sequencing primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200027864-A1.  
 PD 18-MAY-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US26055.  
 XX  
 PR 06-NOV-1998; 98US-0107468.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Tavligian SV, Teng DHF, Simard J, Rommens JM;

```

XX WPI, 2000-376481/32.
XX
XX Human prostate cancer (HPC2) nucleic acids, polypeptides, and
PT antibodies, useful for treatment and diagnosis of prostate cancer -
XX
XX Example 5; Page 60; 157pp; English.
XX
XX The present sequence is a primer used in the isolation of the human
CC and murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC version of the gene is found on chromosome 17p. Some alleles cause a
CC predisposition to cancer, particularly prostate cancer. This gene and its
CC protein can be used in peptide and gene therapy for cancer patients, as
CC well as being useful as diagnostic tools (both for cancer sufferers and
CC those with a predisposition to the disease) and in the production of
CC cancer drugs.
XX
SQ Sequence 41 BP; 13 A; 8 C; 10 G; 10 T; 0 other;
Query Match 0.9%; Score 20.8; DB 21; Length 41;
Best Local Similarity 70.0%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1231 CAACGAAGTCTCTGGAAGAGCTCATGGTGTC 1270
| ||||| ||| ||| ||| ||| ||| |||
Db 41 CTACGACACCACTTTTGAAGATGCTCATGCTGTTCC 2

```

RESULT 38  
 AAS99044/C  
 ID AAS99044 standard; DNA: 41 BP.  
 XX  
 AC AAS99044;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human prostate cancer predisposing gene (HPC2) PCR primer #40.  
 XX  
 KW Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;  
 KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;  
 KW sequencing primer; PCR primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185911-A2.  
 PD 15-NOV-2001.  
 XX  
 PF 07-MAY-2001; 2001WO-US14602.  
 XX  
 PR 05-MAY-2000; 2000US-0564805.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX  
 PI Tavligian SV, Teng DHF, Simard J, Rommens JM;  
 XX  
 WPI, 2002-066599/09.  
 XX  
 PT Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker  
 PT for prostate cancer, is useful in gene therapy techniques to restore  
 PT HPC2 normal levels by which neoplastic growth is suppressed in  
 PT recipient cell -  
 XX  
 PS Example 8; Page 73; 239pp; English.  
 XX  
 XX The invention relates to a human prostate cancer predisposing gene coding  
 CC for an HPC2 polypeptide. The DNA and protein sequences are useful as  
 CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in  
 CC a suspected mutant HPC2 allele by comparing the sequence of the suspected  
 CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also  
 CC useful for detecting an alteration in HPC2, where the alteration is  
 CC associated with cancer in a human. The method involves analysing an HPC2

CC gene or an HPC2 gene expression product from a tissue of the human. The  
 CC HPC2 gene is useful as a marker for prostate cancer and can be used in  
 CC gene therapy techniques to suppress neoplastic growth of recipient cells  
 CC which carry the mutant HPC2 allele. The sequences represent primers used  
 CC in the methods of the invention. cDNA encoding human and mouse HPC2 and  
 CC cDNA encoding HPC2 paralogues and orthologues.

XX Sequence 41 BP; 13 A; 8 C; 10 G; 10 T; 0 other;

Query Match 0.9%; Score 20.8; DB 24; Length 41;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+05;  
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1231 CAACAGAGTGTCTGGAGAAAGCTCATGCTGTCC 1270  
 DB 41 CTACAGACACCACTTTGAAGAGTGTATAGCTTTCC 2

RESULT 39

AAF29312

XX AAF29312 standard; DNA; 48 BP.

XX AAF29312;

XX 18-APR-2001 (first entry)

XX Primer base sequence used to illustrate primer selection method.

XX Primer; optimum sequence; differential display; ss.

XX Synthetic.

XX JP2000308487-A.

XX 07-NOV-2000.

XX 30-MAR-1999; 99JP-0088410.

XX 30-MAR-1999; 99JP-0088410.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2001-046077/06.

XX Selection of primer base for optimizing primer selection comprises

XX obtaining an optimum sequence for differential display from an

XX expression gene data base -

XX Disclosure; Fig 9; 13pp; Japanese.

XX This invention relates to a method for selecting the sequence of a

XX primer. The method comprises obtaining an optimum sequence for a

XX differential display from an expression gene data base, and using the

XX base sequences most frequently expressed as the primer candidates in the

XX order of frequency. The optimum primer group characterised by the use of

XX genetic algorithm from the primer candidates is selected. The method is

XX used for selecting a primer sequence quickly. The present sequence

XX represents a primer used in an illustration of the method of the

XX invention.

XX Sequence 48 BP; 18 A; 2 C; 5 G; 23 T; 0 other;

Query Match 0.9%; Score 20.8; DB 22; Length 48;  
 Best Local Similarity 70.0%; Pred. No. 1.2e+05;  
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1000 TTAATGATCACAATTTTATGCTTGAATATTCAGA 1039  
 DB 3 TTATTTGAAGAAATTTTATTAATGAAGATTCAAA 42

ID ABN71922 standard; DNA; 48 BP.

XX ABN71922;

XX 01-JUL-2002 (first entry)

XX Streptococcus agalactiae PCR primer SEQ ID NO 11362.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

XX group A streptococcus; Streptococcus pyogenes; antibacterial; PCR; ss;

XX antiinflammatory; infection; vaccine; meningitis; gene therapy; primer.

XX Streptococcus agalactiae.

XX Synthetic.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GH04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX Tettelin H;

XX WPI; 2002-352536/38.

XX New Streptococcus protein for the treatment or prevention of infection

XX or disease caused by Streptococcus bacteria, such as meningitis, and

XX for detecting a compound that binds to the protein -

XX Claim 8; Page 4499; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

XX Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS

XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

XX the specification. The proteins have antibacterial and antiinflammatory

XX activity. (1), nucleic acids encoding (1), ABR66044-ABN71526 and

XX antibodies that bind (1) are used in the manufacture of medicaments for

XX the treatment or prevention of infection or disease caused by

XX Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

XX Nucleic acids encoding (1) are used to detect Streptococcus in a

XX biological sample. (1) is used to determine whether a compound binds to

XX (1). A composition comprising (1) or a nucleic acid encoding (1), may be

XX used as a vaccine or diagnostic composition. The disease caused by

XX Streptococcus that is prevented or treated may be meningitis. Nucleic

XX acid encoding (1) may be used to recombinantly produce (1) and may be

XX used in gene therapy. Antibodies to (1) are used for affinity

XX chromatography, immunoassays, and distinguishing/identifying

XX Streptococcus proteins. The present sequence is that of a PCR primer,

XX useful to the invention.

XX Sequence 48 BP; 17 A; 5 C; 11 G; 15 T; 0 other;

Query Match 0.9%; Score 20.8; DB 24; Length 48;  
 Best Local Similarity 70.0%; Pred. No. 1.2e+05;  
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2101 TTTAGATTATTCACAGCTTATTTGAGTAATATTGT 2140  
 DB 44 TATATAAATGTTCACAGCTTATTTGTACAAACTGT 5

RESULT 41

AAT04944/c

ID AAT04944 standard; DNA; 49 BP.

XX

AC	AAT04944;
XX	
DT	05-JUN-1996 (first entry)
XX	
DE	Synthetic promoter operable in B. subtilis and E. coli.
XX	
KW	Plasmid vector; pSM671; promoter; B. subtilis; E. coli;
KM	hydantoinase; carbamylase; alpha-amylase; beta-amylase;
KW	isoamylase; interleukin; interferon; hormones; recombinant;
KW	antibodies; ss.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	-35_signal 15..20
FT	/tag= a
FT	-10_signal 39..44
FT	/tag= b
XX	
PN	EP681027-A2.
PD	08-NOV-1995.
XX	
PF	01-MAR-1995; 95EP-0102876.
XX	
PR	15-APR-1994; 94IT-OMI0727.
XX	
PA	(ENIE ) ENRICERCHE SPA.
XX	
PI	Fraschetti G, Grandi G;
DR	WPL: 1995-375209/49.
XX	
PB	New plasmid vector contg. synthetic promoter for E.coli and
PT	B.subtilis - capable or directing high expression of an heterologous
PI	gene under control of the promoter
XX	
PS	Example 1; Page 9; 14pp; English.
XX	
CC	The plasmid vector pSM671 for the expression of heterologous
CC	proteins, contains AAT0944 which comprises a promoter operable in B.
CC	subtilis and E. coli (AAT0944), the bond site of the mRNA to be
CC	expressed at the ribosome and the multiple cloning site of the
CC	plasmid pUC18. pSM671 is stable in E. coli and B. subtilis, and
CC	the promoter can direct high level expression of heterologous
CC	proteins (over 5% total proteins). The heterologous proteins
CC	include hydantoinase, carbamylase, alpha/beta-amylase, isoamylase,
CC	interleukin, interferon, hormones or recombinant antibodies.
XX	
SQ	Sequence 49 BP; 18 A; 3 C; 6 G; 22 T; 0 other;
XX	
Query Match	0.9%; Score 20.8; DB 16; Length 49;
Best Local Similarity	64.6%; Pred. No. 1.2e+05;
Matches 31: Conservative	0; Mismatches 17; Indels 0; Gaps 0;
OY	2068 AATCGTATAGCTTAATAATATATCAGACTTTTGATTATTCACA 2115
DG	
DG	49 AATCATTTATACATAAAAAATTTTCTGTAAACCAATTAATTTTTTCTA 2
RESULT 42	
AAL29418/c	
ID	AAL29418 standard; DNA; 50 BP.
XX	
AC	AAL29418;
XX	
DT	24-JAN-2002 (first entry)
XX	
DE	Human SNP oligonucleotide #2626.
XX	
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensin; apoptosis related protein; cadherin;

KM	cyclin polymerase; oncogene; histone; kinase; colony stimulating factor;
KM	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin-6-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
XX	nervous system disease; ss.
OS	Homo sapiens.
XX	
PN	MO200147944-A2.
PD	05-JUL-2001.
PF	28-DEC-2000; 200OKO-US35498.
PR	28-DEC-1999; 99US-0173419.
PR	27-DEC-2000; 2000US-0173419.
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
DR	WPI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g.
PT	cancer, autoimmune diseases and infections -
PS	
SS	Claim 1; Page 2137; 4143pp; English.
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotenin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histons, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	a systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
SQ	
	Sequence 50 BP; 15 A; 4 C; 10 G; 21 T; 0 other;
	Query Match            0 %; Score 20.8; DB 22; Length 50;
	Best Local Similarity    64.6%; Pred. No. 1.2e+05;
Matches	31; Conservative     0; Mismatches 17; Indels    0; Gaps      0
OY	
	222 ACAACATGATTGTGAAGAAGCTGGCAATGCATTCATAATTAACAACA 269
Ddb	 50 ACAACATGATTCTTGAATAATATACCAAAATATCTCTATCTGAACTACA 3
RESULT 43	
ID	ABL00257/C
AC	ABL00257 standard; DNA; 50 BP.
XX	
DT	ABL00257;
XX	
DE	05-MAR-2002 (first entry)
XX	
XX	Human silent noncoding SNP oligonucleotide SEQ ID NO:248.
KX	
KW	Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW	immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KV	autoimmune disease; inflammation; cancer; nervous system disease;
KW	infection; polymorphic protein; ds.
XX	
OS	Homo saplens.

XX MO200138586-A2.  
 XX 31-MAY-2001.  
 XX 22-NOV-2000; 2000WO-US32311.  
 XX 24-NOV-1999; 99US-0167383.  
 XX (CURA-) CURAGEN CORP.  
 XX Shinkets RA, Leach M;  
 XX WPI; 2001-355949/37.  
 XX Isolated human nucleic acids comprising one or more single nucleotide  
 XX polymorphisms, useful for treating a subject suffering from a  
 XX pathology, e.g. autoimmune diseases, ascribed to the presence of a  
 XX sequence polymorphism -  
 XX Claim 1; Page 322; 674pp; English.  
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 XX comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 XX to ABB56903 represent human peptides encoded by some of the SNP  
 XX oligonucleotides. The sequences from the present invention can have  
 XX immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
 XX antitubercular activities. Nucleic acids, polypeptides, oligonucleotides  
 XX and antibodies from the present invention can be used for treating a  
 XX subject suffering from, at risk for, or suspected of, suffering from a  
 XX pathology ascribed to the presence of a sequence polymorphism. The  
 XX pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 XX the nervous system, and infection by pathogenic microorganisms. The SNPs  
 XX are also useful for determining which forms of a characterised  
 XX polymorphism are present in individuals. The antibodies may be used in  
 XX the detection, quantitation and/or cellular or tissue localisation of a  
 XX polymorphic protein (e.g., for use in measuring levels of the  
 XX polymorphic protein within appropriate physiological samples).  
 XX Sequence 50 BP; 26 A; 5 C; 7 G; 12 T; 0 other;  
 XX  
 XX Query Match 0.9%; Score 20.8; DB 23; Length 50;  
 XX Best Local Similarity 70.0%; Pred. No. 1.2e+05;  
 XX Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 XX  
 XX QY 2220 AATCTTGATAAATGACTGTTTCTGCTAATACTAA 2259  
 XX 43 AATCTTGATAAATGCTTTTCTGCTCAGATTTA 4  
 XX  
 XX RESULT 44  
 XX ABR6581  
 XX ID ABR6581 standard; DNA; 35 BP.  
 XX ABR6581;  
 XX 24-SEP-2002 (first entry)  
 XX Newcastle disease virus nucleoprotein mutagenic PCR primer P3A.  
 XX Nucleoprotein: NP; immunodominant epitope; newcastle disease; poultry;  
 XX virucide; ND; vaccine; ovo administration; ss; PCR; primer.  
 XX Newcastle disease virus.  
 XX WO200236617-A2.  
 XX 10-MAY-2002.  
 XX 30-OCT-2001; 2001WO-EPI2573.  
 XX 02-NOV-2000; 2000EP-0203814.  
 XX

PA (ALKU ) AKZO NOBEL NV.  
 XX Medabstion T, Koelen MM;  
 XX WPI; 2002-527441/56.  
 XX New Newcastle disease virus (NDV) mutant, useful as a vaccine for  
 XX protecting poultry (e.g. chicken) against Newcastle disease or as a  
 XX marker vaccine to distinguish vaccinated animals from those infected  
 XX with naturally occurring NDV -  
 XX Example 1; Page 15; 51pp; English.  
 XX The invention relates to a Newcastle disease virus (NDV) mutant, which  
 XX lacks an immunogenic epitope on a NDV protein as a result of a mutation  
 XX in a gene encoding the protein, where the NDV mutant lacks an epitope  
 XX located within a regions (amino acids 447-455 and 443-460) of the  
 XX nucleoprotein (NP). Also included are a vaccine against Newcastle disease  
 XX (ND) in poultry comprising the DNA mutant in a live or inactivated form,  
 XX and a pharmaceutical carrier or diluent and determining NDV infection in  
 XX poultry by examining a sample of the animal for the presence or absence  
 XX of antibodies reactive with the immunodominant epitope located within the  
 XX region of the NP. The NDV mutant is useful as a vaccine for protecting a  
 XX poultry against ND. The NDV NP mutant is also useful for manufacturing a  
 XX vaccine against ND in poultry, particularly for in ovo administration.  
 XX The vaccine is also useful in a ND control program to distinguish  
 XX vaccinated animals from animals infected with naturally occurring NDV  
 XX The NDV mutant is also useful as a marker vaccine to allow serological  
 XX distinction between animals vaccinated with conventional vaccine strains  
 XX from that of animals immunised with a vaccine based in this NDV mutant.  
 XX The NDV vaccine is useful in chickens, as well as in other poultry, e.g.  
 XX turkey, pigeons, quails, pheasants, guinea fowl or partridges.  
 XX All currently used whole virus based live and inactivated  
 XX ND vaccines have a major drawback, in that vaccinated animals cannot be  
 XX distinguished from infected animals with standard serological tests  
 XX (e.g. haemagglutination inhibition or virus neutralisation). The present  
 XX NDV immunogenic mutant, being a marker vaccine, enables serological  
 XX differentiation of vaccinated animals from infected animals. The use of  
 XX the present NDV mutant as an embryo vaccine is also proven as effective  
 XX and economical due to the early age of resistance to a specific  
 XX disease. The present sequence represents a PCR primer used to  
 XX delete DNA corresponding to amino acids 442-489 of the nucleoprotein.  
 XX Sequence 35 BP; 12 A; 10 C; 11 G; 2 T; 0 other;  
 XX  
 XX Query Match 0.9%; Score 20.6; DB 24; Length 35;  
 XX Best Local Similarity 74.3%; Pred. No. 1.2e+05;  
 XX Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 XX  
 XX QY 1313 GGCMAAAGATCCCAATGTTGACAAACACACAGC 1347  
 XX 1 GCCAACCCAGAGCCGGGTGATGACAAACCCAGC 35  
 XX  
 XX RESULT 45  
 XX ABR6582/c  
 XX ID ABR6582 standard; DNA; 35 BP.  
 XX ABR6582;  
 XX 24-SEP-2002 (first entry)  
 XX Newcastle disease virus nucleoprotein mutagenic PCR primer P3B.  
 XX Nucleoprotein: NP; immunodominant epitope; newcastle disease; poultry;  
 XX virucide; ND; vaccine; ovo administration; ss; PCR; primer.  
 XX Newcastle disease virus.  
 XX WO200236617-A2.  
 XX 10-MAY-2002.  
 XX

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PF 30-OCT-2001; 2001WO-EP12573.
XX
PR 02-NOV-2000; 2000EP-0203814.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Mebation T, Koolen MJM;
XX
DR WPI; 2002-527441/56.
XX
PT New Newcastle disease virus (NDV) mutant, useful as a vaccine for
PT protecting poultry (e.g. chicken) against Newcastle disease or as a
PT marker vaccine to distinguish vaccinated animals from those infected
PT with naturally occurring NDV
XX
PS Example 1; Page 15; 51pp; English.
XX
CC The invention relates to a Newcastle disease virus (NDV) mutant, which
CC lacks an immunogenic epitope on a NDV protein as a result of a mutation
CC in a gene encoding the protein, where the NDV mutant lacks an epitope
CC located within a regions (amino acids 447-455 and 443-460) of the
CC nucleoprotein (NP). Also included are a vaccine against Newcastle disease
CC (NDV) in poultry comprising the DNA mutant in a live or inactivated form,
CC and a pharmaceutical carrier or diluent and determining NDV infection in
CC poultry by examining a sample of the animal for the presence or absence
CC of antibodies reactive with the immunodominant epitope located within the
CC region of the NP. The NDV mutant is useful as a vaccine for protecting a
CC poultry against ND. The NDV NP mutant is also useful for manufacturing a
CC vaccine against ND in poultry, particularly for in ovo administration.
CC The vaccine is also useful in a ND control program to distinguish
CC vaccinated animals from animals infected with naturally occurring NDV
CC The NDV mutant is also useful as a marker vaccine to allow serological
CC distinction between animals vaccinated with conventional vaccine strains
CC from that of animals immunised with a vaccine based in this NDV mutant.
CC The NDV vaccine is useful in chickens, as well as in other poultry, e.g.
CC turkey, pigeons, quails, pheasants, guinea fowl or partridges.
CC All currently used whole virus based live and inactivated
CC ND vaccines have a major drawback, in that vaccinated animals cannot be
CC distinguished from infected animals with standard serological tests
CC (e.g. haemagglutination inhibition or virus neutralisation). The present
CC NDV immunogenic mutant, being a marker vaccine, enables serological
CC differentiation of vaccinated animals from infected animals. The use of
CC the present NDV mutant as an embryo vaccine is also proven as effective
CC and economical due to the early age of resistance to a specific
CC disease. The present sequence represents a PCR primer used to
CC delete DNA corresponding to amino acids 442-489 of the nucleoprotein.
XX
SQ Sequence 35 BP; 2 A; 11 C; 10 G; 12 T; 0 other:
XX
Query Match 0.9%; Score 20.6; DB 24; Length 35;
Best Local Similarity 74.3%; Pred. NO. 1.2e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1313 GGCAGAAAAGATCCCAATGTTGACAAACACAGC 1347
DB 35 GGCAGACGAGAGCGCGGTGATGACAAACCCAGC 1

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OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT variation replace(24,6)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN M09954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
XX
PS Claim 1; Page 677; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 13 A; 18 C; 11 G; 5 T; 0 other:
XX
Query Match 0.9%; Score 20.6; DB 21; Length 47;
Best Local Similarity 74.3%; Pred. NO. 1.4e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1872 GCCACCTCACCAGAGACCTTGAGAGCAGCAGGAC 1906
DB 1 GTCACCTCACCAGAGAGGAGCAGACGCTAGGAC 35

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RESULT 46
ID AAZ67746 standard; DNA; 47 BP.
XX
XX AAZ67746;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2093.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX

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RESULT 47
ID AAL30421/c
XX
XX AAL30421 standard; DNA; 50 BP.
XX
XX AAL30421;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3629.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX

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XX OS Homo sapiens.
XX PN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000MO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
XX PR 27-DEC-2000; 2000US-0173419.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX PT cancer, autoimmune diseases and infections -
XX PS Claim 1; Page 2428; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
XX CC G-protein coupled receptors and thioesterases. The present sequence is
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX CC by them may be used in the prevention, diagnosis and treatment of
XX CC diseases associated with inappropriate expression of the proteins listed
XX CC above. Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX CC leukemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms.
XX SQ Sequence 50 BP; 15 A; 13 C; 7 G; 15 T; 0 other;
Query Match 0.9%; Score 20.6; DB 22; Length 50;
Best Local Similarity 74.3%; Pred. No. 1.4e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2201 AAGATGCTGTTACTTTTGATTCGTGAATGA 2235
DB 37 AGGAGTGTGTGATTTTTCGATTCGACAAAGA 3
RESULT 48
AAI79057/C
ID AAI79057 standard; DNA: 50 BP.
XX AC AAI79057;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:5998.
XX OS Homo sapiens.
XX PN WO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000MO-US32758.

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XX PR 30-NOV-1999; 99US-0168138.
XX PR 29-NOV-2000; 2000US-0726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy -
XX PS Claim 1; Page 2345; 2653pp; English.
XX CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
XX CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
XX CC AAM53114 to AAM53329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (1) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides.
XX CC For example, (1) may be used to treat disorders by rectifying mutations
XX CC or deletions in a patient's genome that affect the activity of
XX CC polypeptides by expressing inactive proteins or to supplement the
XX CC patient's own production of polypeptide. Additionally, (1) and its
XX CC complementary sequences may also be used as DNA probes in diagnostic
XX CC assays to detect and quantitate the presence of similar nucleic acids
XX CC in samples, and therefore which patients may be in need of restorative
XX CC therapy. The polypeptides encoded by (1) may be used as antigens in the
XX CC production of antibodies specific for polymorphic polypeptides. The
XX CC antibodies may also be used to down regulate expression and activity.
XX CC The antibodies may also be used as diagnostic agents for detecting the
XX CC presence of polymorphic polypeptides in samples.
XX SQ Sequence 50 BP; 26 A; 4 C; 16 G; 4 T; 0 other;
Query Match 0.9%; Score 20.6; DB 22; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.4e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1093 CTTTCGTGCTGCTCTTTGTTCTCTGAATTTTCAGACACTTT 1135
DB 43 CTTTCCTGCTCTGCTCTCTTTCTTTCTTTTTCATAGAACTCT 1
RESULT 49
AAV68378/C
ID AAV68378 standard; DNA: 50 BP.
XX AC AAV68378;
XX DT 10-MAR-1999 (first entry)
XX DE Clone #4 fragment identified by CAG repeat analysis method.4.
XX OS Homo sapiens.
XX PN WO9849345-A1.
XX PD 05-NOV-1998.
XX PF 29-APR-1998; 98WO-US08616.
XX PR 29-APR-1997; 97US-0045078.
XX PA (UYBO-) UNIV BOSTON.
XX PI Smith CL;

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